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July 30, 2005, 15:25:34; Search time 257.941 Seconds (without alignments) 4108.047 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                  nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*			SUMMARIES		
Result No.	Score	Query	Query Match Length DB	DB	ΙD	Description	Ħ
-	42.2	23.6	270	. 5	AAA89399	Aaa89399 S	Scorpion
7	40.8	22.8	270	ហ	AAA89400	Aaa89400 S	Scorpion
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c 10	32	17.9	780	4	ABA89006		Escherich
11	32	17.9	2489	9	ABS78877	Abs78877 E	E. coli C
12	32	17.9	2489	10	ADH80444	Adh80444	Adh80444 Escherich
13	32	17.9	2498	4	ABA89004	Aba89004 E	Escherich
c 14	32	17.9	2811	4	ABL25174	Ab125174 D	Drosophil
c 15	31	17.3	4590	Ŋ	AAH24065	Aah24065 Y	Yeast AOD
16	30.6	17.1	582	9	ABN63438	Abn63438 H	Human can
17	30.4	17.0	13563	4	ABL06306	Ab106306 D	Drosophil
18	30.4	17.0	13629	4	ABL06290	Ab106290 D	Drosophil
19	30.2	16.9	473	m	AAC98441	Aac98441 H	Human col
20	30.2	16.9	1037	4	AAH34174	Aah34174 H	Human col

Claim 1(a); Page 57; 60pp; English.

21 30.2 16.9 3144 13 ADR08046 22 30.2 16.9 3379 10 AD899514 24 30.2 16.9 3379 10 AD899514 25 30.2 16.9 3379 10 AD895514 26 30.2 16.9 3379 12 ADC1247 27 30.2 16.9 3379 13 ADE54323 28 30.2 16.9 3379 13 ADE54323 29 30.2 16.9 3406 6 ABK6479 31 30.2 16.9 3406 6 ABK6479 32 30.2 16.9 3406 6 ABK6479 33 30.2 16.9 3445 10 ADC12594 34 30.2 16.9 3445 10 ADC12594 35 30.2 16.9 3445 10 ADC12594 36 30.2 16.9 3445 10 ADC12594 37 30.2 16.9 345 10 ADC12594 38 30.2 16.9 345 10 ADC12594 39 30.2 16.9 345 10 ADC12594 30 30.2 16.9 3466 8 ARX50301 30 30.2 16.9 38643 10 ADR37749 30 30.2 16.9 38643 10 ADC18515 30 30 30 30 30 30 30 30 30 30 30 30 30 3	Adr08046 Full leng	Aak99410 DNA of AP	Adb99514 Human MCM	Adb31296 Testoster	Ado19247 Human PRO		Adp23357 PRO polyp	4	-		Abn95130 Gene #162	Ach03947 Human cDN	Adjs6503 Human cDN	Adl12594 Human ste	Aas95018 Human DNA	Acc51032 Human bla	Abx76294 Lung canc	Ada03011 Mouse Ncf	Adb72749 Mouse Ncf	Adc85491 Mouse Ncf	Adm74606 Murine ca	Abk39306 DNA encod	Acall635 Human lun	Aca02821 Lung canc	Adh46863 Human lun	
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New isolated polynucleotide encoding a scorpion toxin for treating epilepsy, degenerative disorders such as Huntington's disease, and neuronal death following stroke, and for creating plants that are insect-tolerant. Scorpion; venom; toxin; sodium channel agonist; anticonvulsant; nootropic; cerebroprotective; insecticide; ss. Scorpion sodium channel agonist cDNA clone ibj1c.pk008.f14. Ε. Location/Qualifiers BP. (DUPO) DU PONT DE NEMOURS & CO Wong JF; 21-JUN-2000; 2000WO-US017048. AAA89399 standard; cDNA; 270 99US-0140410P. (revised)
(first entry) 1. .63 /*tag= a 64. .267 /*tag= a Hottentotta judaica. Herrmann R, Lee J, WPI; 2001-050111/06. P-PSDB; AAB20077 WO200078957-A2 22-JUN-1999; 11-SEP-2003 23-APR-2001 28-DEC-2000. sig_peptide mat_peptide AAA89399; RESULT 1

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The present sequence is that of a portion of the cDNA insert in clone inbjic.pk008.f14 that encodes a protein showing 29.64 identity to an insecticidal toxin of Orthochirus scrobiculosus. The clone was isolated from a scorpion (Buthotus judaicus) telson cDNA library. The invention provides isolated nucleic acid sequences (see AAA89386-400) encoding scorpion toxins (see AAB20664-78) that are soddium channel modifiers. The invention also relates to the construction of a chimeric gene encoding all or part of the sodium channel modifier, in sense or antisense or attentation, where expression of the chimeric gene results in production of altered levels of the sodium channel modifier in a transformed host cell. Sodium channel modifiers can be used to treat neurological problems involving abnormal functioning of excitory amino acid synapses, e.g. epilepsy, Huntington's disease and neuronal death following stroke. Genetically engineered recombinant baculoviruses which express protein toxins capable of incapacitating an insect host can be used as biological insecticides. The uncleic acids can be used to create transgence plants in which sodium channel agonists of the invention are expressed for improved insect tolerance. (Updated on 11-SEP-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.2; DB 5; Length 270;
Pred. No. 0.00012;
0; Mismatches 43; Indels C
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l Similarity 61.3%;
68; Conservative (
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P-PSDB; AAB20078.
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23-APR-2001
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The present sequence is that of a portion of the cDNA insert in clone inbjc.pk008 119 that encodes a protein showing 29.6% identity to an insecticidal toxin of Orthochirus scrobiculosus. The clone was isolated from a scorpion (Buthotus judaicus) telson cDNA library. The invention provides isolated nucleic acid sequences (see AAA89386-400) encoding scorpion toxins (see AAB2064-78) that are soddum channel modifiers. The invention also relates to the construction of a chimeric gene encoding all or part of the sodium channel modifier, in sense or antisense or antisense or antisense of all or part of the sodium channel modifier, in sense or antisense contentation, where expression of the chimeric gene results in production of altered levels of the sodium channel modifier in a transformed host cell. Sodium channel modifiers can be used to treat neurological problems involving abnormal functioning of excitory amino acid synapses, e.g. capilepsy, Huntington's disease and neuronal death following stroke. Genetically engineered recombinant baculoviruses which express protein toxins capable of incapacitating an insect host can be used as biological in which sodium channel agonists of the invention are expressed for improved insect tolerance. (Updated on 11-SEP-2003 to standardise OS
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New isolated polynucleotide encoding a scorpion toxin for treating epilepsy, degenerative disorders such as Huntington's disease, and neuronal death following stroke, and for creating plants that are insect-
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                                                                                                        Claim 1(a); Page 58; 60pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 22.8%; Score 40.8; DB 5; Length 270; Local Similarity 61.1%; Pred. No. 0.00038; es 66; Conservative 0; Mismatches 42; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scorpion sodium channel agonist cDNA clone ibj1c.pk0004.h3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 270 BP; 82 A; 34 C; 58 G; 96 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                   Claim 1(a); Page 57; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA89397 standard; cDNA; 270 BP.
                          Wong JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .63
/*tag= a
64. .267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                          Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hottentotta judaica.
                                                                                                   P-PSDB; AAB20076
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23-APR-2001
                          Herrmann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
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                                                                                                                                                                                                                                   tolerant
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ID AAA,
XX ACA AAA
XX ACA AAA
DT 11-
DT 23-
XX SC KW SCC
XX SC KW NOC
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The present sequence is that of a portion of the cDNA insert in clone inscrictal towin of orthochirus scrobiculosus. The clone was isolated insecticidal towin of orthochirus scrobiculosus. The clone was isolated from a scorption (buthotus judaicus) telson cDNA library. The invention provides isolated nucleic acid sequences (see AAA89386-400) encoding corputation toxins (see AAA80064-78) that are sodium channel modificars. The invention also relates to the construction of a chimeric gene encoding all or part of the sodium channel modifier, in sense or antisense contentation, where expression of the chimeric gene results in production of altered levels of the sodium channel modifier in a transformed host call. Sodium channel modifiers can be used to treat neurological problems involving abnormal functioning of excitory amino acid synapses, e.g. epilepsy, Huntington's disease and neuronal death following stroke.

Call sodium channel secondaring a insect host can be used so biological insecticides. The nucleic acids can be used to create transgenic plants in miproved insect tolerance. (Updated on 11-SEP-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide encoding a scorpion toxin for treating epilepsy, degenerative disorders such as Huntington's disease, and neuronal death following stroke, and for creating plants that are insect-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AATCCGGACTGCATTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 TTCCAATGCTGGTGTGAATTTCTGAAGGATGAGAACGTGAAGGTCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 ACCTCGTGTTGGTGTGAATATTTGAAAAAGAAGACATCGATATTT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.2%; Score 38; DB 5; Length 270, 56.0%; Pred. No. 0.0039; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 270 BP; 84 A; 33 C; 57 G; 96 T; 0 U; 0 Other;
                                                                                                            Ε.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1(a); Page 56; 60pp; English.
                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                   Wong JF;
21-JUN-2000; 2000WO-US017048.
                                                    99US-0140410P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat persephin cDNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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ses 93; Conservative
                                                                                                                                                                   Herrmann R, Lee J,
                                                                                                                                                                                                                     WPI; 2001-050111/06
                                                                                                                                                                                                                                                     P-PSDB; AAB20075.
                                                    22-JUN-1999;
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98WO-US019163

15-SEP-1998;

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                                                                                                                                                                                                                                                          This sequence comprises a fragment of rat persephin cDNA. Persephin is a novel member of the glial-derived neurotrophic factor-neurturin family. The clone was obtained by PCR amplification using primers (see AAT90797-98) based on an isolated fragment (see AAT90796) of rat persephin cDNA. A full-length rat persephin gene (see AAT90805) was subsequently obtained. Mouse and rat persephin polypeptides (see AAW30064-68), and DNA sequences encoding them, are used in claimed methods for preventing or treating neuronal degeneration, haematopoietic cell degeneration and cardiac muscle degeneration or insufficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                   GDNF-neurturin family related growth factor, Persephin - used to prevent or treat cellular, neuronal or non-neuronal, degeneration or insufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth factor; GF; persephin; neuron growth; cellular degeneration; peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma; brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neurturin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTTGATTCTTCCGACAATACCTACCTGTGCGCCCCCTTTGGGAGATAATCCGGACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.2%; Score 32.6; DB 2; Length 336;
Best Local Similarity 52.6%; Pred. No. 0.37;
Matches 71; Conservative 0; Mismatches 64; Indels C
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 336 BP; 77 A; 91 C; 98 G; 70 T; 0 U; 0 Other;
                                                                                                                                      Lampe PA;
                                                                                                                                      Kotzbauer PT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial sequence of rat persephin cDNA.
                                                                                                                                                                                                                                       Example 12; Page 157; 228pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX60455 standard; DNA; 336 BP
                                                            97WO-US003461.
                                                                                   96US-00615944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 GGTCATCAAGGAAGG 151
                                                                                                                                      Johnson EM, Milbrandt JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                             (UNIW ) UNIV WASHINGTON.
                                                                                                                                                             WPI; 1997-470818/43
            WO9733911-A1
                                                            14-MAR-1997;
                                                                                     14-MAR-1996;
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                                    18-SEP-1997
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WO9914235-A1

25-MAR-1999

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The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and growth of neurons and non-neuronal cells. The persephin GF polypeptides or polymucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g. neuronal degeneration resulting from desence parkinson's disease, Huntington's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumours, multiple sclerosis, or infection, hematopoietic cell degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiences, cardiac muscle degeneration or insufficiency resulting from desing e.g. peripheral nerve traums or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The Gr can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persephin by a population of cells. The products can also be used for detection and diagnosis
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                                                                                                                                                                                                                                                                                                          New isolated persephin growth factor nucleic acids used to, e.g. promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor; GF; persephin; neuron growth; cellular degeneration; peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma; brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neurturin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 CACTTGATTCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 caccricaccriricaaaccreccriricaricaricricacacacaccaccic
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                                                                                                                                   Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 336 BP; 77 A; 91 C; 98 G; 70 T; 0 U; 0 Other;
                                                                                                                                   Lampe PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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                                                                                                                                   Kotzbauer PT,
                                                                                                                                                                                                                                                                                                                                                                                                          Example 12; Page 156; 222pp; English
97US-00931858
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                                                                                                                                   Milbrandt JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 52.6 tes 71; Conservative
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                                                               (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                      WPI; 1999-244023/20.
                                                                                                                                                                                                                                                                                                                                             neuronal growth
16-SEP-1997;
                                                                                                                                                                   Desauvage F;
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                                                                                                                                   Johnson
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Milbrandt JD,
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nes 71; Conservative
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                                                                                                                                                                                                                                                                                      WPI; 1999-244023/20.
                                                                                                                                                                                                                                                                                                                                  neuronal growth.
                                                                                                                                                                15-SEP-1998;
                                                                                Unidentified
                                                                                                           WO9914235-A1
                                                                                                                                                                                                                                                            Desauvage F;
                                                                                                                                      25-MAR-1999
                                                                                                                                                                                                                                              Johnson EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337
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ABZ53533
ID ABZ5:
XX
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                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and or polypeptides or polymerical properties or polymerical mand non-neuronal cells. The persephin GF polypeptides or polymerical neuropathy, anyotrophic lateral sclerosis. Alzheimer's degeneration or insufficiency, e.g. neuronal degeneration resulting from peripheral neuropathy, anyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumours, multiple selerosis, or infection, hematopoletic cell degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, anily exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persephin by a population of cells. The products can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 TTAAGATCTGTCAGAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 TTCAGCCACCACAGCCACAAGCTGCGGCTGAGAGCTGAGGCAGCTGCTGCTGCAATGGTGGT 166
                                                                                                                                                                                                                               isolated persephin growth factor nucleic acids used to, e.g. promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTTGATTCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCA 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor; GP; persephin; neuron growth; cellular degeneration;
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                                                                                                                                                                Klein R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.2%; Score 32.6; DB 2; Length 336; 52.6%; Pred. No. 0.37; tive 0; Mismatches 64; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 336 BP; 77 A; 91 C; 98 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                Kotzbauer PT, Lampe PA,
                                                                                                                                                                                                                                                                         Example, Page 159; 222pp; English
                                                                                98WO-US019163
                                                                                                          97US-00931858
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                                                                                                                                                               Milbrandt JD,
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Matches 71; Conservative
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                                                                                                                                                                                                                                              neuronal growth
                         WO9914235-A1
                                                                                                                                                               Johnson EM,
Desauvage F;
                                                                                                          16-SEP-1997;
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The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and crowth of neurons and non-neuronal cells. The persephin GF polypeptides or proventh of neurons and non-neuronal cells. The persephin GF polypeptides or polymore or insufficiency, e.g. neuronal degeneration resulting from degeneration or insufficiency, e.g. neuronal degeneration resulting from caripheral neuropathy, anyotrophic lateral sclerosis, Alzheimer's disease, parkinson's disease, Horntongon's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumours, misufficiency resulting from eosinopenia, anemias, thrombocytopenia, or them-cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiences, cardiac muscle degeneration or insufficiency resulting from eosinopenia, tramma or injury, exposure to resulting from cardiomyopathy or congestive heart failure. They can also be used for treating a eigense such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for neurotoxins, metabolic diseases such as diabetes or renal dysfunctions medium. The antisense polymucleotides can be used for treating a disease condition mediated by expression of persephin by a population of cells.

The products can also be used for detection and diagnosis
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peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma; brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neurturin; ss.
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                                                   ABZ53533 standard; cDNA; 515 BP.
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The invention relates to a library of DNA fragments of Bacherichia colistrains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and encoded proteins (ABB52495-ABB52994 ABB52994) of nature B2/D-A-. The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. colinfections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli particularly an extra-intestinal infection that include systemic and non-diarrhocal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pathogenic; Escherichia coli CPT073 infection; livestock; pyelonephritis; urinary tract infection; open reading frame; ORF; uropathogenic; antibacterial; aropathic; nephrotropic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of nature B2/D+
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                                                        immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephritis; antibiotic resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 TCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATC
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                              Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clermont O, Nassif X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDICALE
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Pred. No. 0.84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Fig 6; 646pp; English.
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Best Local Similarity 58.3
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bingen E, Bonacorsi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-550253/61
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                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                       W0200166572-A2
                                                                                                                                                                                                                                                                                                                       13-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS78877
ID ABS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, olid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising profitess of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTGAATTTCTGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 GTCTCGTCGGTGAGGAATTGGGGAAGTGCTATGCGCGCGAGGGCGTGAATCATTTGGAGA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 CCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATCTGTC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of expression of specific Aspergillus genes for monitoring the fermentation and growth conditions of the fungus, using DNA probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horiuchi H;
Abe K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2646; 48pp + Sequence Listing; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 515 BP; 124 A; 138 C; 135 G; 118 T; 0 U; 0 Other;
                                                                                                                                                      Aspergillus oryzae, fermentation; fungus; industrial; EST;
                                                                                      Aspergillus oryzae polynucleotide SEQ ID NO 2646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \kita O, Kashiwagi Y, Kitamoto K,
Kobayashi T, Kitamoto N, Gomi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INST ADVANCED IND SCI & TECHNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NORQ ) NAT FOOD RES INST MIN AGRIC.
                                                                                                                                                                                           expressed sequence tag; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RES INST BREWING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2002; 2002WO-IB000890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001JP-00098371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTGTGGGGCTTTGA 326
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                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akita O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-046817/04.
                                                                                                                                                                                                                                                       Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                   WO200279476-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Machida M,
Takeuchi M,
                          28-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAAD-)
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ABA89006/C
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AC ABA890
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Escherichia coli CFT073 nucleic acid

CFT073, useful for preparing a or preventing infection caused by

Burland VD;

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TCTGGCGCCAATACGTCCCTGACCATCAGAGCCGAGTGTAAAAATGATGGCATCAATATC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of nature B2/D+
                                                                                                                                                                                  molecule. The nucleic acid is useful for preparing a composition for diagnosing, treating or preventing infection caused by Escherichia coli CFT073. The present sequence represents a contig of the Escherichia coli CFT073 genome that is not present in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a library of DNA fragments of Escherichia coli strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature
                                                                                                                                                                                                                                                                                                                                                         33 TCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia;
                                                                                                                                                                                                                                                                                             17.9%; Score 32; DB 10; Length 2489; 58.3%; Pred. No. 1.3;
                                                                                                                                                                                                                                                              Sequence 2489 BP; 668 A; 563 C; 578 G; 677 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCAGAAACACGGTGTGGATTACGGGTATTGCTAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCGGTAAATCGGTAAGTGTTTCAGGTATTGAAAC 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli polynucleotide SEQ ID NO 578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyelonephritis; antibiotic resistance; ds
                                                                            acid of Escherichia coli
for diagnosing, treating
                                                                                                                                                                     The invention relates to an isolated molecule. The nucleic acid is useful
                                                                                                                                       Claim 1; SEQ ID NO 44; 4pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 6; 646pp; English.
                                                                              New nucleic acid of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA89004 standard; DNA; 2498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-2000; 2000FR-00003145.
02-FEB-2001; 2001FR-00001449.
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                          Escherichia coli CFT073.
                 Welch RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonacorsi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI, 2001-550253/61.
                                              WPI; 2003-863698/80
                                                                                                                                                                                                                                                                                                           Local Similarity
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                 Blattner FR,
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                                                                                               composition
                                                                                                                                                                                                                                                                                                                           26;
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                                                                                                                                                                                                                                                                                                                                                                                         901
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                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                        The present invention relates to polynucleotide sequences from the genome of the pathogenic Escherichia coli strain CFT073. Almost all the sequences present in E. coli CFT073 are absent in the previously sequenced laboratory strain K-12. The polynucleotide sequences of the invention are useful for preventing, diagnosing or treating E. coli CFT073 infection in humans or livestock. The polynucleotide sequences are useful for preventing urinary tract infections and pyelonephritis. Likewise, the polypeptides encoded by the different open reading frames (ORF1-5) are useful for generating a vaccine against uropathogenic E. coli strains. ABS78034-ABS79085 represent genomic sequences from E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 reregececannecrecercarearecencarecearerananareareacarearene 960
                                                                                                                                                                                                                                New DNA sequences of the pathogenic Escherichia coli CFT073 strain, useful for preventing or treating E. coli CFT073 infection in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; Echerichia coli; CFT073; Escherichia coli CFT073 infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2489 BP; 668 A; 563 C; 578 G; 677 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 6; Length 2489; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                             Claim 1; Page 141-142; 765pp; English
                                                                                                                                                                     Burland VD,
                                                                                                                                       (WISC:) WISCONSIN ALUMNI RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADH80444 standard; DNA; 2489 BP
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                                                                          19-OCT-2001; 2001WO-US046833
                                                                                                         2000US-0242412P
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                                                                                                                                                                     Welch RA,
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BURLAND V D.
                                                                                                                                                                                                   WPI; 2002-691532/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                 WO200259320-A2.
                                                                                                         19-OCT-2000;
                                                                                                                                                                     Blattner FR,
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                                            01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                livestock
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Best Local S
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Tinsley

Nassif X,

Clermont O,

Sequence 2811 BP; 719 A; 640 C; 660 G; 792 T; 0 U; 0 Other;

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B2/D+A-. The polynucleotides have potential antiinflammatory, antibacterial and immunosupressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. colinfections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGGCGCCCAATACGTCCCTGACCATCGAGTGTAAAAATGATGGCATCAATATC 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATC
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 2498 BP; 673 A; 563 C; 580 G; 682 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 4; Length 2498;
Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                   broad spectrum antibiotics
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                          Human growth hormone analogue peptide; hGH; AOD9604; lipid metabolism; modulation; lipolysis stimulation; hormone-sensitive lipase stimulation; lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity; functional food; transgenic yeast; fat/lean ratio; food use; ds.
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DB 4; Length 2811;
                   40; Indels
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Score 32; DB 4
Pred. No. 1.4;
                   0; Mismatches
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                                                                                                                           RESULT 15
AAH24065/c
ID AAH24065 standard; DNA; 4590 BP.
17.9%;
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Query Match
                   Matches
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The invention relates to novel transgenic organisms useful in the production of functional food and drink products for the treatment or prevention of obseity via the regulation of lipid metabolism. The crapable of stimulating the activity of hormone-sensitive lipase (the key enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key enzyme in lipogenesis). The growth hormone fragment preferably contains at least the disulphide-bonded loop of a mammalian growth hormone (but is not the full-length growth hormone) and is optionally linked to an epitope tag or heterologous fusion protein partner. The transgenic organism may be a microorganism used to produce a fermented product (e.g., yeast), or an edible plant or animal or cell thereof. Food or drink made using methods of the invention are used to modify fat/lean ratio, ilpid metabolism or food use in a mammal. In particular, the food or drink products may be used to treat or prevent obseity, particularly in humans, and may also be used to improve the fat/lean ration of the invention, the human growth hormone (hGH) fragment analogue ADD9604 was expressed in yeast, optionally fused to the FIAG epitope (AAB73625). The present sequence is described as a DNA sequence from yeast in the sequence listing, but is not further referred to in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New organisms containing nucleic acid encoding a growth hormone fragment which modulates lipid metabolism are useful to produce dietary aids for obesity and in the meat production industry.
*tag= o notes as * in the specification"
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/note= "Represented as * in the specification"
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note= "Represented as * in the specification"
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12.7%; Pred. No. 3.9;
tive 65; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 48-50; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               Belyea CI, Ng FM, Vaughan P,
                                                                                                                                                                                                                                                                                06-NOV-2000; 2000WO-AU001362.
                                                                                                                                                                                                                                                                                                                          99AU-00003875.
                                                                                                                                                                                                                                                                                                                                                                     (META-) METABOLIC PHARM LTD
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Best Local Similarity 12.77
Matches 14, Conservative
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                                        misc_feature
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55 GCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGTGTGGATŢ 114

0; Gaps

115 ACGGGTATTGCTACGCCTTCCAATGCTGTGTGAATTTCTGAAGGATGAG 164

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Search completed: July 30, 2005, 18:28:44 Job time : 264.941 secs

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MEDLINE-21518524; PubMed=11606203;

WEDLINE-21518524; PubMed=11606203;

MEDLINE-21518524; PubMed=11606203;

A Inceglu B., Lango J., Wu J., Hawkins P., Southern J., Hammock B.D.;

IT "Isolation and characterization of a novel type of neurotoxic peptide

IT "Isolation and characterization of a novel type of neurotoxic peptide

IT "Isolation and characterization of a novel type of neurotoxic peptide

IT Subthidae0.";

Eur. J. Blochem. 268:5407-5413(2001).

C -1- FUNCTION: Binds to sodium channels and inhibits the inactivation

CC (By similarity). Moderately toxic, but very high abundant. Lethal

CC -1- FUNCTION: Donot target reptilian channels.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUB SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parabuthus transvaalicus (South African fattail scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Parabuthus.
NCBI_TaxID=170972;
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InterPro; IPR002061; Scorpion_toxinL.
Pfam; PF00537; Toxin_3; 1.
Probom; PD0009089; Scorpion toxinL; 1.
Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Sodium channel inhibitor; Toxin.
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Pred. No. 2.4e-18;
8; Mismatches 15; Indels
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By similarity.
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Last sequence update)
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Last annotation update)
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SCCE_CENLL
SC2B_CENLL
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SCXC_CENLL
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O68PH2
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(Rel. 41, Last seq
(Rel. 44, Last ann
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     Similarity
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28-FEB-2003
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05-JUL-2004 (05-JUL-2004)
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Gapop 10.0 , Gapext 0.5
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Beta-toxin (Fragment)
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       Toxin KBT precursor....., Les aunotation update)
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centruroides noxius (Mexican scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
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PDB, 1PE4, NMR, A=1-67.
3D-structure, Direct protein sequencing, Ionic channel inhibitor; Neurotoxin, Sodium channel inhibitor; Toxin.
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5298A578F1A62905 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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25-0CT-2004 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
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9274 MW;
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80 AA;
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67 AA;
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TISSUE=Venom;
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Bukaryota, Metazoa, Arthusopda, Chelicerata, Arachnida, Scorpiones,
Buthida, Buthoidea, Buthidae, Centruroides.

NCBI_TaxID=218467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthida, Buthoidea, Buthidae, Centruroides.
                                                                                                                                         4 YPLASNGCKFGCSGLGENNPTCNHVCEKKAGSDYGYCYAWTCYCEHVAEGTV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
EMBL; AY351301; AAR08036.1; -.
HSSP; P01493; 1JZA.
                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                      7 YPLDSSDNTYLCAPLGD-NPDCIKICOKH-GVDYGYCYAFOCWCEFLKDENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 YLVNSTGCKYGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPE 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YPLDSSDNTYLCAPLGDNPDCIKIC--QKHGVDYGYCYAFQCWCEFLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 64;
     Length 67;
37.0%; Score 127; DB 1; Length 67
46.2%; Pred. No. 3.1e-07;
tive 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhu S.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA
GO; GO:0005515; F:protein binding; IEA.
GO; GO:000552; P:defense response; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   730092293C661C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.9%; Score 123; DB 2;
46.9%; Pred. No. 8.7e-07;
tive 6; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2004 (Rel. 44, Last annotation update)
Toxin CSE MI (CSEMI) (CSEIII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 AA
                                                                                                                                                                                                                                                                                         64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Centruroides sculpturatus (Bark scorpion)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003614; Knott.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR001219; Neurotoxin.
Ffam; PF00537; Toxin 3; 1.
PRINTS; PR00285; SCORPNTOXIN.
PRINTS; PR00284; TOXIN.
ProDom; PD001908; Scorpion_toxinL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom;
MEDLINE=93162874; PubMed=1286943;
Pete M.J., Conlon J.M., Murphy R.F.;
                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                      PRT;
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Ewing.";
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primary structure of a potent toxin from the venom of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Centruroides noxius (Mexican scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                               HSSP; PO1495; ICN2.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR001219; Scorpion_toxinL.
Féan; PP00537; Toxin 3; 1.
PRINTS; PR00284; SCORPNTOXIN.
PRINTS; PR00284; TOXIN.
PRODOM; PD0009098; Scorpion toxinL; 1.
Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Sodium channel inhibitor; Toxin.
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Pred. No. 4.4e-06;
5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLCAPLGDNPDCIKIC-QKHGVDYGYCYAFQCWCEFLKDENV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 YECLKLGDNDYCLRECRQQYGKSGGYCYARACWCTHLYEQAV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
By similarity.
By similarity.
56BDA312F17D3C9C CRC64,
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GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0008202; F:defense response; IEA.
GO; GO:0008405; P:pathogenesis; IEA.
InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 AA; 6929 MW; 8300977935D08A91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00537; Toxin 3; 1.
PRINTS; PR00265; SCORBNTOXIN.
PPCDOm; PD000908; Scorpion_toxinL; 1.
SWART; SM00505; Knoct; 1.
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ilarity 46.9%;
Conservative
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Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
  "Isolation and
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SEQUENCE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Procedin Sci. 11:479-486 (2002).
-!- FUNCTION: Bainds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom gland.
-!- TISSUB SPECIFICITY: Belongs to the alpha/beta-scorpion toxin family. Beta-toxin subfamily:
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Venom gland;
MEDLINE=21486965; PubMed=11600153; DOI=10.1016/S0041-0101(01)00174-X;
Corona M., Valdez-Cruz N.A., Merino E., Zurita M., Possani L.D.;
"Genes and peptides from the scorpion Centruroides sculpturatus Ewing, that recognize Na(+)-channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babin D.R., Watt D.D., Goos S.M., Mlejnek R.V.; Amino acid sequences of neurotoxic protein variants from the venom of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND DISULFIDE BONDS.
MEDLINE=21836430; PubMed=11847271; DOI=10.1110/ps.39202;
Cook W.J., Zell A., Watt D.D., Ealick S.E.;
"Structure of variant 2 scorpion toxin from Centruroides sculpturatus
                                                                                                                                  SCX2 CENSC STANDARD; PRT; 87 AA.
P01433; Q95WC2; Q95WC3; Q95WC4; Q95WC5; Q95WC8;
21-JUL-1986 (Rel. 01, created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
Neurotoxin 2 precursor (CSEV2) (CSE V2).
Centruroides Sculpturatus (Bark scorpion).
Bukaryota; Metacoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-structure; Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Signal; Sodium channel inhibitor; Toxin. SIGNAL 119
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS CSEV2A; CSEV2A*; CSEV2B; CSEV2C AND
23
                     7 YPLDSSDNTYLCAPLGDNPDCIKIC -- QKHGVDYGYCYAFQCWCEFLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Centruroides sculpturatus Ewing.";
Arch. Biochem. Biophys. 164:694-706(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurotoxin 2.
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InterPro; IPR002061; Scorpion_toxinL.
Pfam, PP00237; ToxinI.3; 1.
PRINTS; PR00285; SCORPNTOXIN.
PRINTS; PR00284; TOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000908; Scorpion toxinL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom;
MEDLINE=75163395; PubMed=4460885;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF338457; AAL23425.1; -. EMBL; AF338458; AAL23426.1; -. EMBL; AF338459; AAL23427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1JZA; X-ray; A/B=20-85.
PDB; 1JZB; X-ray; A=20-85.
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HELIX
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"Amino acid sequences of neurotoxic protein variants from the venom of
Centruroides sculpturatus Baning";
Arch. Biochem. Biophys. 164:694-706(1974).
                                                                                                                                                                                                                                                                                                              [1]

SEQUENCE FROM N.A. (ISOFORMS CSEV3B AND CSEV3B*).

TISSUB-Venom gland;

MEDLINE=21466965; Pubmed=11600153; DOI=10.1016/S0041-0101(01)00174-X;

COrona M., Valdez-Cruz N.A., Merino E., Zurita M., Possani L.D.;

"Genea and peptides from the scorpion Centruroides sculpturatus Ewing, that recognize Na(+)-channels.";

Toxicon 39:1893-1898(2001).
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                              SCX3_CENSC STANDARD; PRT; 87 AA.
P01494; Q95WB9; Q95WC0;
21-JUL-1986 (Rel. 01, Created)
21-SPED-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last sequence update)
Neurotoxin 3 precursor (CBEV3) (CBE V3).
Centruroides sculpturatus (Bark scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=82200153; PubMed=7080025; DOI=10.1016/0041-0101(82)90137-4;
                                                                                                                                                                                         .;
3
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Unpublished results, cited by:
Fontecilla-Camps J.-C., Almassy R.J., Suddath F.L., Bugg C.E.;
Toxicon 20:1-7(1982).
                         I -> M (in C8Ev2B and C8Ev2D).
LELI -> PALV (in C8Ev2A*).
K -> R (in C8Ev2B).
G -> A (in C8Ev2D).
C -> A (in C8Ev2D).
CDK -> NKC (in Ref. 2).
SC -> CS (in Ref. 2).
                                                                                                                                                                           Score 117; DB 1; Length 87; Pred. No. 6e-06; 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND DISULFIDE BONDS.
                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                    53
                                                                                                                                                                                                            33 YGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPE 72
                                                                                                                                                              9520 MW; 760810C65269B74E CRC64;
                                                                                                                                                                                                    16 YLCAPLGDNPDCIKIC -- QKHGVDYGYCYAFQCWCEFLKD
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 20-84 (ISOFORM CSEV3A).
                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom;
MEDLINE=75163395; PubMed=4460885;
                                                                                                                                                                           Query Match
Best Local Similarity 52.5%;
Matches 21; Conservative
 NCBI_TaxID=218467;
                                                                                                                                                              87 AA;
 DISULPID
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DISULPID
                         VARIANT
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Secreted (By similarity).
-1- SINILARITY: Belongs to the alpha/beta-scorpion toxin family.
EMBL; AY351306; AAR08041.1;
-- HSSP; P01493; 1JZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 YPLDSSDNTYLCAPLGDNPDCIKIC--OKHGVDYGYCYAFQCWCEFLKD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 116; DB 2; Length 64;
Pred. No. 5.7e-06;
4; Mismatches 20; Indels
                                                                                                                                            GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:000552; F:defense response; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                  64 AA; 7137 MW; 8EBEFD8934D78C47 CRC64;
                                                                                                                                                                                                                            InterPro; IPR003614; Knott.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR001219; Neurotoxin.
Fam; PR00537; Toxin 3; 1.
PRINTS; PR00285; SCORPNTOXIN.
PRINTS; PR00284; TOXIN.
ProDom; PD001908; Scorpion_toxin1; 1.
SWART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.8%;
Best Local Similarity 46.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
NCBI_TaxID=218467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                    NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6V4Y7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6V4Y7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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7
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                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Centruroides sculpturatus (Bark scorpion).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthida, Buthoidea, Buthidae, Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                         Centruroides noxius (Mexican scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
NCBI_TaxID=6878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Secreted (By similarity).
-1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
EMBL; AV351310; AAR08045.1; -.
HSSP; P01493; 1JZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 YPLDSSDNTYLCAPLGDNPDCIKIC-QKHGVDY-GYCYAFQCWCEFLKDENV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
7
                                                                                                                                                  2;
                                                                                                             34.1%; Score 117; DB 1; Length 87; 52.5%; Pred. No. 6e-06; tive 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008200; F:ion channel inhibitor activity; IEA.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:000552; P:defense response; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                    33 YGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPE 72
                                                                                                                                                                               16 YLCAPLGDNPDCIKIC--OKHGVDYGYCYAFQCWCEFLKD 53
                                                                              761857AB95031A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AA; 7382 MW; 01A24DF96C24FCC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06V4Y4;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-toxin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

33.8%; Score 116; DB 2;
Best Local Similarity 42.3%; Pred. No. 5.7e-06;
Matches 22; Conservative 10; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003614; Knot1.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR002061; Scorpion_toxinL.
Pfam. PF00537; Toxin 3; 1.
PRINTS; PR00285; SCORPNTOXIN.
PRINTS; PR00284; TOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roDom; PD000908; Scorpion toxinL; 1.
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                              9480 MW;
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-toxin (Fragment).
                                                                                                                              Best_Local Similarity
Matches 21; Conserv
                                                                            87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                              SEQUENCE
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                  Q6V4Y0;
                             STRAND
                                                                                                                                                                                                                                                                                                Q6V4Y0
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                                             TURN
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Gaps

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Centruroides noxius (Mexican scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
NCBI_TaxID=6878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
EMBL; AY351303; AAR08038.1; -.
HSSP; P01493; 1JZA.
52
4 YLVKSDGCKYDČFWLĠENEGĊDKEĊKAKNQĠGSYĠYĊYAFAĊŴĊEGLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 115; DB 2; Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GG; GO:0005576; C:extracellular; IEA.
GG; GO:0005200; F:ion channel inhibitor activity; IEA.
GG; GO:0005515; F:protein binding; IEA.
GG; GO:0005525; P:protein binding; IEA.
GG; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR002061; Scorpion_toxinL.
InterPro; IPR002061; Scorpion_toxinL.
IPRINTS; PR002865; SCORPNTOXIN.
IPRINTS; PR002865; SCORPNTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu S.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7050 MW; DEBFFAD255D08A8D CRC64;
                                                                                                                                                                                                                        05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Beta-toxin (Fragment).
                                                                                                                                                              64 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000908; Scorpion_toxinL; 1.
SMART; SM00505; Knot1; 1.
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060444 110 AC 110 DT DT DT 0 0 DT OS 0 0 D

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the activated channels, thereby blocking neuronal transmission
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25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Cex11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q68PG4;
                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               068PG4
                                                                                                                                                                                                                                                                                                          loxin
                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                          Valdez-Cruz N.A., Davila S., Licea A., Corona M., Zamudio F.Z.,
Carcia-Valdes J., Boyer L., Possani L.D.;
Carcia-Valdes J., Boyer L., Possani L.D.;
The Spicohemical, genetic and physiological characterization of venom
The Spicohemical of Scorphons: Centruroides exilicauda Wood
The Centruroides sculpturatus Ewing.";
Biochimie 0:0-012004).
C-1- SIMCELLULAR LOCATION: Secreted (By similarity).
C-1- SIMCELLULAR LOCATION: Secreted (By similarity).
C-1- SIMCIANITY: Belongs to the alpha/beta-scorpion toxin family.
C-1- SIMCIANITY: Belongs to the alpha/beta-scorpion toxin family.
C-1- SIMCIANITY: Rocia December Company of Co.000405; P.Pathogenesis; IEA.
C-1- SIMCIANITY: PRO0361; Scorpion_toxin.
C-1- SIMCIANITY: PRO0285; SCORPHOXIN.
C-1- SIMCIANITY: PRO0285; SCORPHOXIN.
C-1- SIMCIANITY: PRO0284; TOXIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corona M., Possani L.D.;
Corona M., Possani L.D.;
"Genes and poptides from the scorpion Centruroides limpidus limpidus,
"Genes and poptides from the scorpion Centruroides limpidus,
that recognize Na(+)-channels.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Binds to sodium channels and inhibits the inactivation
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
NCBI_TaxID=6879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Sodium-channel modifier neurotoxin Cll7 precursor.
Centruroides limpidus limpidus (Mexican scorpion).
Bukaryota, Metazoa; Arthropoda, Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
              2
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                                                           4 YLVNSTGCKYGCFWLGKNEGCDKECKAKNQGGSYGYCYAFGCWCEGLPE 52
                                         7 YPLDSSDNTYLCAPLGDNPDCIKIC--QKHGVDYGYCYAFQCWCEFLKD 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 115; DB 2; Length 73; Pred. No. 8.5e-06; 3; Mismatches 15; Indels
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 AA; 8045 MW; EE9165045BCA25BF CRC64;
                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 YLCAPLGDNPDCIKICQKHGVDYGYCYAFQCWCEFLKD 53
              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 YNCYILGKNKYCNSECKEVGAGYGYCYAFGCWCEGLPE
  Pred. No. 7.4e-06;
              5; Mismatches
                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 AA
                                                                                                                                              73
                                                                                                                                                                                                                                              Centruroides exilicauda (Bark scorpion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000908; Scorpion_toxinL; 1.
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
46.98;
                                                                                                                                                                                                                   Cex13 neurotoxin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 52.6%;
hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00505; Knot1; 1.
Neurotoxin.
              23; Conservative
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                      25-OCT-2004 (TrEMBLrel.
 Similarity
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=29941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CENTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
 Best Local
                                                                                                                                            Q68PG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
SCX7_CENLL
                                                                                                                RESULT 12
Q68PG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
              Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00505; Knot1; 1. -
Ionic channel inhibitor; Neurotoxin; Signal; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sodium-Channel modifier neurotoxin Cll7.
By similarity.
By similarity.
By similarity.
792E0B0E73618134 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthida, Buthoidea, Buthidae, Centruroides.
NCBI_TaxID=6879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUB SPECIFICITY: Expressed by the venom gland.
--- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1;
9.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 YLCAPLGDNPDCIKICQKHGVDYGYCYAFQCWCE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 115; DB Pred. No. 9.9e-5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 YICWKLGENKYCIDECKEIGAGYGYCYGFGCYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Centruroides exilicauda (Bark scorpion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
                                                                                                                                                                                                                                                                        EMBL; AF491133; AAP49508.1; -.
InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
Pfam; PF00537; Toxin_3; 1.
ProDom; PD000908; Scorpion_toxinL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000908; Scorpion_toxinL; 1. SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR0013614; Knotl.
InterPro; IPR001219; Neurotoxin.
InterPro; IPR001061; Scorpion_toxinL.
Pfam; PF00537; Toxin 3; 1.
PRINYS; PR00288; SCORPNTOXIN.
PRINYS; PR00284; TOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            19
82
82
58
63
63
9621 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 28, (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cex11 neurotoxin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AA;
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Valdez-Cruz N.A., Davila S., Licea A., Corona M., Zamudio F.Z.,
Valdez-Cruz N.A., Davila S., Licea A., Corona M., Zamudio F.Z.,
Garcia-Valdes J., Boyer L., Possani L.D.,
"Biochemical, genetic and physiological characterization of venom
components from two species of scorpions: Centruroides exilicauda Wood
and Centruroides sculpturatus Ewing.";
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Centruroides exilicauda (Bark scorpion).
Eukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1. SUBCELLULAR LOCATION: Secreted (By similarity).
-1. SUBCELLULAR LOCATION: Secreted (By similarity).
-1. SUBLARITY: Belongs to the alpha/beta-scorpion toxin family.
BMBL; AY649866; AAT97999.1; -.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR003614; Knot1.
InterPro; IPR00319; Neurotoxin.
FIGHERPRO; PR0022061; Scorpion_toxinL.
PRINTS; PR00285; SCORPNTOXIN.
PRINTS; PR00284; TOXIN.
PRINTS; PR00284; TOXIN.
PRODOM; PR000908; Scorpion_toxinL; 1.
SWART; SW00505; Knot1; 1.
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Pred. No. 1.3e-05;
4; Mismatches 12; Indels
                                                                      Score 113; DB 2; Length 66;
Pred. No. 1.3e-05;
4; Mismatches 12; Indels
  1 1
66 AA; 7549 MW; 975598FF9BF84F36 CRC64;
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67 AA; 7637 MW; 8705B5222B898E86 CRC64;
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Cex8 neuctoxin (Fragment).
                                                                                                                                                                         16 YLCAPLGDNPDCIKICQKHGVDYGYCYAFQCWCE 49
                                                                                                                                                                                                        14 YSCWLLGENEYCIAECKEIGAGYGYCHGFGCWCE 47
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                                                                                                                                                                                                                                                                                                                                                    67 AA.
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                                                                        32.9%;
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Best Local Similarity 52.9%;
Matches 18; Conservative
                                                                      Query Match
Best Local Similarity 52.99
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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NON TER
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YSCWLLGENEYCIAECKEIGAGYGYCHGFGCWCE 48

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Search completed: July 8, 2005, 15:33:03 Job time : 179 secs

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122 GCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
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Patent No. 5756340
OTHER INFORMAT
OTHER INFORMAT
FEATURE:
NAME/KEY: CDS
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US-08-435-040-1
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LENGTH: 723
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Sequence 6862, Ap
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10269, A
10480, A
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-435-040-1
US-08-941-964-1
US-08-941-936-1
US-08-991-916-1
US-09-902-540-58
US-08-676-166A-1
US-08-472-053-43
US-08-265-429A-4
PCT-US95-09069-1
US-08-265-429A-1
PCT-US95-09069-1
US-09-373-272-2
US-09-373-272-2
US-09-373-272-2
US-09-373-272-2
US-09-373-272-2
US-09-36-301A-1008
US-09-252-991A-1008
US-09-252-991A-10690
US-09-252-991A-10690
US-09-902-540-9650
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                                                                                                                                                                                       US-10-617-978-17_COPY_73_249
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                                                                                                                                                            Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1269
3404
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Sequence 2, Appli
Sequence 1, Appli
Sequence 3712, Ap
Sequence 1180, Ap
Sequence 10956, Ap
Sequence 11255, A
Sequence 11255, A
 Sequence 178, App
Sequence 10367, A
Sequence 10706, A
Sequence 10462, A
Sequence 4964, App
Sequence 444, App
Sequence 1244, App
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Sequence 4633, Ap
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| Sequence 1, Application US/10152296 |
| Patent No. 6723537 |
| GENERAL INFORMATION: |
| APPLICANT: Peelle Beau |
| APPLICANT: Peelle Pharmaceuticals, Incorporated |
| TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells |
| TITLE REPERENCE: 021044-000110US |
| CURRENT APPLICATION NUMBER: US/10/152,296 |
| PRIOR FILING DATE: 2002-12-10 |
| PRIOR PILING DATE: 2001-05-18 |
| PRIOR FILING DATE: 2001-05-18 |
| NUMBER OF SEQ ID NOS: 2 |
| SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGACGTGCCAGGGAACTACCCGCTGGACAGCTCGGACAACACCTTGTGCGCACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.6; DB 4; Length 723;
Pred. No. 0.011;
0; Mismatches 79; Indels
US-09-016-434-178
US-09-252-991A-10367
US-09-252-991A-10462
US-09-252-991A-10462
US-09-902-549-016-444
US-09-999-016-444
US-09-999-016-444
US-09-902-540-1244
3 US-09-103-840A-1
3 US-09-103-840A-1
US-09-902-540-1180
US-09-902-540-3036
US-09-902-540-3036
US-09-252-991A-110255
US-09-252-991A-110255
                                                                                                                                                                                                                                                                                       US-09-103-840A-2
US-09-103-840A-1
US-09-902-540-4633
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Best Local Similarity 53.0%;
Matches 89; Conservative 0
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   263 4
1206 4
1208 4
1509 4
1909 4
1410529 4
1410529 4
1008 4
1008 4
1101 4
4403765 4
486 4
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; OTHER INFORMATION: DGRED
US-10-152-296-1
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
            APPLICANT: Hamook, Bruce D.
APPLICANT: Hamook, Bruce D.
APPLICANT: Harmann, Rafael
APPLICANT: Moskowitz, Haim
TITLE OF INVENTION: Insect Control With Multiple Toxins
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1450
CITY: San Franciso
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4121
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: SALENTIN Release #1.0, Version #1.25
SOFTWARE: PAPLICATION NUMBER: US/08/435,040
FILING DATE: 08-MAY-1995
CURSSIFICATION: SALENTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1; Length 285;
Pred. No. 0.023;
0; Mismatches 40; Indels
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APPLICANT: Herrmann, Rafael
APPLICANT: Herrmann, Rafael
APPLICANT: Moskowitz, Haim
TITLE OF INVENTION: Insect Control With Multiple Toxins
NUMBER OF SQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1450
CITY: San Franciso
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE LOCKET NUMBER: 25.00.078USO
TELECOMMUNICATION INFORMATION:
TELERAX: (415) 362-556
TELERAX: (415) 362-556
TELERX: 278638 MGPS
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERIFICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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US-09-020-216-1
; Sequence 1, Application US/09020216
; Patent No. 6162430
; GENERAL INFORMATION:
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l Similarity 61.5%;
64; Conservative (
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COUNTRY: U.S.A.
ZIP: 94111-4121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity
Matches 64; Conserva
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GENERAL INFORMATION:
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APPLICANT: Tatsumi, Hiroki
APPLICANT: Eisaki, Nacki
APPLICANT: Bisaki, Nacki
APPLICANT: Horiuchi, Tatsuo
APPLICANT: Horiuchi, Tatsuo
APPLICANT: Nagahara, Ayumu
TITLE OF INVENTION: Pyruvate Orthophosphate Dikinase Gene,
TITLE OF INVENTION: Recombinant DNA, and Process For Producing Pyruvate
TITLE OF INVENTION: Orthophosphate Dikinase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 ACAGCTCGGACAACACCTACCTGTGCGCACCCCTGGGCGACAACCCGGACTGCATCAAGA 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 TCTGCCAGAAGCACGGCGTCGACTACGGCTACGCGTTC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 ACTGCACCAAGAACGCCCCCAACTCTGGCTACTGCCAATGGTTC 189
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,216
                                                                                                    PEPLICATION NUMBER: US/US/US/LIE
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 08-WAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2500.078USO
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 362-548
TELEFAX: (415) 362-5418
TELEFAX: 278638 MGPS
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MONGECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1997
N: 435
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Patent No. 6054305
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US-09-902-540-58/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2535 GATCGGCCTCGACTACGTCTCCTGCTCGCCGTTCCGCATTCCGGTGGCCCGGCTGGAGG 2593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERRICE. 38-10[15849]B
CURRENT APPLICATION NUMBER: 108/19/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 GGGAACTACCCGCTGGACAGCTCGGACAACACCTACCTGTGCGCACCCCTGGGCGACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.0%; Score 39; DB 3; Length 2634;
58.0%; Pred. No. 0.089;
ive 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 CAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HIRAKI-03009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-705-8410
TELEPAK: 415-397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERS STICS:
LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                               ORGANISM: Microbispora thermorosea STRAIN: IFO 14047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6862, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Myxococcus xanthus
US-09-902-540-6862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.0
Best Local Similarity 58.0
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: 1..2634
US-08-941-936-1
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RESULT

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Sequence 58 Application US/09902540

Sequence 58 Application US/09902540

Sequence 58 Application US/09902540

SERVERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Miegand, Roger C.

TILLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: 60/217,883

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR PILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 58

LIENGTH: 618
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APPLICANT: Parish, John H.
TITLE OF INVENTION: EXPLOITATION OF THE CELLULASE COMPLEX OF
TITLE OF INVENTION: NEUROSPORA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.8%; Score 38.6; DB 4; Length 618; nilarity 52.9%; Pred. No. 0.075; Conservative 0; Mismatches 74; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEB: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 CAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 AACGGCTTCGGCCAGTTCGTCGTGGAGATGAACCCCA 283
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 15-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 1321-1-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08676166A
Patent No. 5955270
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
: USA
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STATE: New Jerse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
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89 TTACGGCGCCAGCTACGCTACTGCTGGACCTGGGGCCTTGCTGCTGCGAGGGCT 148
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                                                                                                                                                                                                                                                                                                                                                                                                39 CAACACCTACCTGTGCGCACCCCTGGGCGACAACCCGGGCTGCATCAAGATCTGCCAGAA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4. Application US/08265429A
Patent No. 5677151
GENERAL INFORMATION:
APPLICANT: Wilson, David B.
APPLICANT: Zhang, Sheng
TITLE OF INVENTION: Thermostable Cellulase From A Thermomonospora Gene NUMBER OF SEQUENCES:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
                                                                                                                                                                                                                                                                                                                                                                                                                                             29 CGACGGCTGCAAGGTGGCTTGCCTGATCGGCAACGAGGGCTGCGACGAAGAAGGTGCAAGGAGTGCAAGG
                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 0.24;
0; Mismatches 43; Indels 0
                                                                                                                                                                                                                                                ch 21.5%; Score 38; DB 4; Length 197; 1 Similarity 61.4%; Pred. No. 0.079; 81; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BULIALO
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYBE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: BM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUWBER: US/08/265,429A
FILING DATE: 24/06/94
CLASSIFICATION WHORER: 18617.0008
FILING DATE: A106/94
CLASSIFICATION WINBER: 35,300
REFERENCE/DOCKET NUMBER: 36,300
REFERENCE/DOCKET NUMBER: 18617.0008
FELEPHONE: (716)856-4000
TELLEPHONE: (716)856-4000
TELLEPRA: 716-049-0349
INPORMATION FOR SEQ ID NO: 4:
                                                                                                       ; TYPE: DNA
; ORGANISM: Leuirus quinquestriatus hebraeus
US-08-472-053-43
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 43 LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermomonospora fusca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 59.4%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1269 nucleotides
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MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 GAAGGACGAGAA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 GCCGGACGACAA 160
                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1800 Or
CITY: Buffalo
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XX36
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US-08-265-429A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-08-265-429A-4
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                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACTGCTACGCGTTCCAGTG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 Gráciacagadariacacacrágacacacagacia de procesor de contra de c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 CTACCCGCTGGACAGCTCGGACAACACCTGTGCGCACCCCCTGGGCGACAACCCGGA 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.6%; Score 38.2; DB 2; Length 1849; Best Local Similarity 52.9%; Pred. No. 0.14; Matches 82; Conservative 0; Mismatches 73; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning sequencing and homologies of the CBH-1 (exocellobiohydrolase) gene of Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT ZLOTKIN, ELIAHU
APPLICANT: MAEDA, SUSUMU
APPLICANT: MACUTCHEN, BILLY F.
APPLICANT: MCCUTCHEN, BILLY F.
APPLICANT: HAMOCK, BRUCE D.
APPLICANT: HAMOCK, BRUCE D.
APPLICANT: BELAGAPE, RAMA M.
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
FILE REFERENCE: UCOS8 1FWCP2
CURRENT APPLICATION NUMBER: US/08/472,053
CURRENT APPLICATION NUMBER: 08/229417
PRIOR APPLICATION NUMBER: 07/62963
FRIOR FILING DATE: 1994-04-15
PRIOR FILING DATE: 1994-04-15
PRIOR FILING DATE: 1994-12-19
PRIOR FILING DATE: 1994-12-19
PRIOR FILING DATE: 1998-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TITLE: crassa
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1849
US-08-676-166A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
join(152..832, 892..1758)
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Patent No. 6689356
GENERAL INFORMATION:
                                                                                                                                                                                                                                                ORGANISM: Neurospora crassa
STRAIN: Oak Ridge 74A
IMMEDIATE SOURCE:
                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                        LENGTH: 1849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 892..>1761
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
<152..832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: Taleb, F
AUTHORS: Radford, A
TITLE: Cloning seque
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833..891
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CLONE: X
FEATURE:
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
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US-08-472-053-43
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; Sequence 1, Application US/08265429A
; Patent No. 5677151
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                         GCCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACTGC 123
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                                                                     454 GGCGGCACCGAGCTCTGCGCCTACATGAAGCAGAACGGCGGCTACGTCAACGGTGTCGGC 513
                                                                                                                                                                                                                                                                                                                                                                                                                         Thermostable Cellulase From A Thermomonospora Gene
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                                                                                                                                                                  514 TACGCCCTCCGCAAGCTGGGCGAGATCCCGAACGTCTACAACTACA 559
                                                                                                                         124 TACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514 TACGCCCTCCGCAAGCTGGCGAGATCCCGAACGTCTACAACTACA 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Hodgson, Russ, Andrews, Woods & Goodyear
1800 One M&T Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 08/265,429
FILING DATE: 24/06/94
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 18617.0008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: Maccompatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09069
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.0%; Score 37.2; DB Best Local Similarity 59.4%; Pred. No. 0.24; Matches 63; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                         Sequence 4, Application PC/TUS9509069
GENERAL INFORMATION:
APPLICANT: Wallson, David B.
APPLICANT: Walker, Larry P.
APPLICANT: Zhang, Sheng
TITLE OF INVENTION: Thermostable Cell
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOGGSON, Russ, Andrews,
STREET: 1800 One MkT Plaza
CITY: Buffalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermomonospora fusca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 716-849-0349
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1269 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE: bacterium
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RESULT 11 US-08-265-429A-1

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APPLICANT: Wilson, David B.
APPLICANT: Walker, Larry P.
APPLICANT: Walker, Larry P.
APPLICANT: Zhang, Sheng
TITLE OF INVENTION: Thermostable Cellulase From A Thermomonospora Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9509069
GENERAL INFORMATION:
APPLICANT: Wilson, David B.
APPLICANT: Larry P.
APPLICANT: Zhang, Sheng
TITLE OF INVENTION: Thermostable Cellulase From A Thermomonospora Gene
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 TACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Indels
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STREET: 1800 One M&T Plaza
CITY: Buffalo
                                                                                                                                                                                                                                   STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,429A
FILING DATE: 24/06/94
CLASSIPECATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.0%; Score 37.2; DB 1; Best Local Similarity 59.4%; Pred. No. 0.32; Matches 63; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REPERENCE/DOCKET NUMBER: 18617.0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (716)856-4000
TELEPAX: 716-849-0349
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 3404 uncleosides
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : New York
RY: United States
14203-2391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-265-429A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
PCT-US95-09069-1
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1547 GGCGGCACCGAGCTCTGCGCCTACATGAAGCAGAACGCGGGCTACGTCAACGGTGTCGGC 1606
64 GGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACTGC
                                                                                                                                                   1607 racecerceceaecreseceaericeceaacercracacraca 1652
                                                                                                      124 TACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
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; Sequence 2, Application US/09373272
; Patent No. 6818803
; GENERAL INFORMATION:
; APPLICANT: Austin-Phillips, Sandra
; APPLICANT: Bugges, Richard D
; APPLICANT: German, Thomas L
; APPLICANT: Ziegelhoffer, Thomas
; TITLE OF INVENTION: Lignocellulosic-Degrading Enzymes
; TITLE OF INVENTION: Lignocellulosic-Degrading Enzymes
; FILE REFERENCE: Transgenic Plants Expressing Cellulase
; CURRENT APPLICATION NUMBER: US/09/373,272
; CURRENT FILING DATE: 1999-08-12
; EARLIER FILING DATE: 1997-06-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
: LENGRIH: 3503
; TURNER OF SEQ ID NOS: 33
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                                                                                                                                                             PILING DATE:
CLASSIFICATION:
PRICR APPLICATION:
PRIOR APPLICATION NUMBER: U.S. Serial No. 08/265,429
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 18617.0008
REGISTRATION NUMBER: 18617.0008
TELERENCE/ODCKET NUMBER: 18617.0008
TELERENCE/ODCKET NUMBER: 18617.0008
TELERENCENCATION INFORMATION:
TELERENCE (716/856-4000
TELEREX: 716-849-0349
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TOWATH: 3404 NUCleotides
                          MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1 SOFTWARE: Wordperfect for Windows 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY.
MOLECULE TYPE: Genomic ....
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3404 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Thermomonospora fusca
US-09-373-272-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: YX36
CELL TYPE: bacterium
       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-09069-1
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US-09-373-272-2
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90 CIGCCAGAAGCACGGCGTCGACTACGGCTACGCGTTCCAGTGTTGGTGCGAGTT 149
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Sequence 22, Application US/08866340
Patent No. 6020318
GENERAL INFORMATION:
APPLICANT: Szyf, Moshe
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani, Shyam
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE. ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

20.7%; Score 36.6; DB 3; Length 394;
Best Local Similarity 53.1%; Pred. No. 0.25;
Matches 78; Conservative 0; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/866,340
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                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                            STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTY: A
COUNTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Keom, Wayne A.
REGISTRATION NUMBER: 33,923
REPERENCE/DOCKET NUMBER: 106.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 394 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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US-09-103-875-28
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Sequence 28, Application US/09103875A
Patent No. 6221849
GENERAL INFORMATION:
APPLICANT: Sayf, Moshe
APPLICANT: Biggy, Pascal
APPLICANT: Ramchandani, Shyam
TITLE OF INVENTION: DIA METHYLITRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
TITLE OF INVENTION: DIAGONUCLEOTIDES
TITLE OF INVENTION: DIAGONUCLEOTIDES
TITLE OF INVENTION: DIAGONUCLEOTIDES
TITLE REFERENCE: 10610.1.94
CURRENT APPLICATION NUMBER: US/09/103,875A
CURRENT PILING DATE: 1988-06-24
EARLIER PILING DATE: 1987-12-17
EARLIER FILING DATE: 1997-12-17
EARLIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PATENTING UNCONS: 138
LENGTH: 394
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; ORGANISM: Homo sapiens
US-09-103-875-28
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Search completed: July 30, 2005, 20:19:26 Job time: 100.522 secs

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July 30, 2005, 15:25:34; Search time 255.059 Seconds (without alignments) 4108.047 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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177
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Maximum Match 100%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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geneseqn2003ds:*
geneseqn2004as:*
geneseqn2004bs:*
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3: geneseqn2008:*

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5: geneseqn20018s:*

6: geneseqn20018s:*

7: geneseqn20018s:*

9: geneseqn20038s:*

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Maximum DB seq length: 200000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aad46281 Discosoma	Aad46278 Discosoma	Aad46282 Discosoma	Aad28208 Discosoma	Aad28207 Discosoma	Aad28209 Discosoma	Adc24128 Discosoma	Ad146207 Discosoma	Adc24134 Discosoma	Adl46205 Human cod	Ad146225 Human cod	Aaa48743 Humanised	Adn33980 Mutant-ty	Abz22476 Mammalian	Adl18131 RFP:PS(NI	Adl18155 RFP:PS(HI	Ads75466 Fibrohexa	Ads75468 Fibrohexa	Adq91220 Fusion co	Aal47954 Modified
SUMMARIES	ΩI	AAD46281	AAD46278	AAD46282	AAD28208	AAD28207	AAD28209	ADC24128	ADL46207	ADC24134	ADL46205	ADL46225	AAA48743	ADN33980	ABZ22476	ADL18131	ADL18155	ADS75466	ADS75468	ADQ91220	AAL47954
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	Query Match	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.5
	Score	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6	41.6
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                                                                                    The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as subscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) mutant DNA of the invention
New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant of an aggregating Chidarian chromo- or fluorescent protein or mutant for analyte detection assays or fluorescence activated cell sorting
                                                                                                                                                                                                                                                                                                                 CCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCG 265
                                                                                                                                                                                                                                                                                                                                          TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                                                                                                 266 AGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGCGGCGGCGTGGCGACCGTGACCC 325
                                                                                                                                                                                                                                                                                          Fluorescent protein; chromoprotein; protease cleavage assay; filter; fluorescenc activated cell sorting application; fluorescent timer; biosensor; fluorescente resonance energy transfer application; FRET; colouring agent; recombinant DNA application; analyte detection assay; sunscreen; second messenger detector; drFP583 protein; NFP-6; gene; ds
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                                                                                                                                                                                                                                       ch 23.5%; Score 41.6; DB 6; Length 675; Similarity 53.0%; Pred. No. 0.44; 89; Conservative 0; Mismatches 79; Indels (
                                                                                                                                                                                                                 Seguence 675 BP; 142 A; 227 C; 204 G; 102 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                79; Indels
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/product= "drFP583 wild-type protein"
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                                                              Disclosure, Page 73; 80pp; English
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04-DEC-2001; 2001US-00006922.
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The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is a DNA encoding Discosoma sp. drFP583 (NFP-6) wild-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Length 678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 678 BP; 146 A; 223 C; 203 G; 106 T; 0 U; 0 Other;
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/product= "drFP583 mutant protein, E5-NA"
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Pred. No. 0.44;
0; Mismatches
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                                                                                                                                                      Disclosure; Page 70; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.0%;
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04-DEC-2001; 2001US-00006922.
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les 89; Conserv
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                                                                                                   applications.
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Matches
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The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer proteins are useful in monitoring the activity of a promoter, determining the age of a protein, identifying an agent that modulates the activity of a promoter and in the fluorescent timer proteins are also useful for assessing gene expression during development of a multicellular organism or during expression during development of a multicellular organism or during collular differentiation, in response to a drug or other inducer of promoter activity, as a reporter to serve as a read-out of promoter activity, as a reporter to serve as a read-out of promoter activity or protein stability, to investigate temporal aspects of the activity of a regularory element, for determining cell fate during development and organ remodelling, in spatial and temporal in distinguishing between newly formed and pre-existing structures, e.g. membrane junctions and extracellular matrix components. The fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            timer proteins may further be used to investigations where photobleaching techniques are employed, as detectable labels, as selectable markers, as biosensors in proteavened markers, as selectable markers, as selectable markers, as selectable markers, as assays, and as second messenger detectors. The nucleic acids can be used to generate transgenic, non-human plants or animals or site-specific gene modifications in cell lines. The present sequence is a cond encoding Discosoma sp. Es fluorescent protein derived from humanised wild-type Anthozoa protein drFP583 by substituting val to Ala at 105 and Ser to Thr
                                                                                                                                                    New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 AGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGCGACCGTGACCC 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Discosoma sp. humanised wild-type Anthozoa protein drFP583 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 aggacrecrecerecaggacgerecricareracaaggrearica 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 678 BP; 147 A; 224 C; 203 G; 104 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.5%; Score 41.6; DB llarity 53.0%; Pred. No. 0.44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                      Disclosure, Fig 2; 89pp; English.
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                                                                           WPI; 2002-154595/20.
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les 89; Conserv
                                                                                                         P-PSDB; AAE17541
                                                                                                                                                                                                                                     stability
                             Fradkov AF,
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Matches
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                                                                                                                                                                                                                                                                                                                                                         The invention relates to nucleic acid molecules encoding non-aggregating chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are useful in analyte detection assays, as colouring agents, as markers in recombinant DNA applications, as sunscreens or filters, in fluorescence prokaryotic and eukaryotic cells, in screening assays, as second messenger detectors, in fluorescence activated cell sorting applications, in protease cleavage assays or as fluorescent timers. The present sequence is Discosoma sp. drFP583 (NFP-6) mutant DNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CCGACGTGCCAGGGAACTACCCGCTGGACAGCTCGGACAACACCTTACCTGTGCGCACCCC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                            'nucleic acid encoding a non-aggregating chromo- or fluorescent mu
an aggregating Cnidarian chromo- or fluorescent protein or mutant
lyte detection assays or fluorescence activated cell sorting
                                                   Savistky A, Fradkov A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 41.6; DB 6; Length 678; 53.0%; Pred. No. 0.44; ive 0; Mismatches 79; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 678 BP; 145 A; 225 C; 203 G; 105 T; 0 U; 0 Other;
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                                             Yanushevich Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Disclosure; Page 73; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD28208 standard; cDNA; 678 BP.
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/product=
                                                   Lukyanov K,
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CLONTECH LAB INC.
                                                                                                   2002-691654/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                              P-PSDB; AAE28837
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                                                                                                                                                                                                                                                                applications
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                                                      Lukyanov S,
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Key

Matches

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Gaps

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79;

AAD28209 standard; cDNA; 678 BP.

4AD28209

22-APR-2002 (first entry)

AAD28209;

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New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking
                             /*tag= a
/product= "Humanised wild-type Anthozoa protein drFP583"
               Location/Qualifiers
1. .678
                                                                                                                                                                                                    Example 1; Fig 1; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                generating fluorescent proteins
                                                                                13-JUN-2001; 2001WO-US019097.
                                                                                               14-JUN-2000; 2000US-0211607P.
                                                                                                            (CLON-) CLONTECH LAB INC.
                                                                                                                           Fradkov AF, Terskikh A;
                                                                                                                                          WPI; 2002-154595/20.
                                                                                                                                                 P-PSDB; AAE17540.
                                                   WO200196373-A2
 Discosoma вр
                                                                                                                                                                                     stability
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The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer protein are useful in monitoring the activity of a promoter, determining the act seekin in controling a population of cells comprising a fluorescent timer protein. The fluorescent timer proteins are also useful for assessing gene expression during development of a multicellular organism or during expression during development of a multicellular organism or during cellular differentiation, in response to a drug or other inducer of promoter activity, as a reporter to serve as a read-out of promoter activity, as a reporter to serve as a read-out of promoter activity, as a reporter to serve as a read-out of promoter activity, or protein stability, to investigate temporal approtein approximation of newly synthesised proteins and accumulated proteins, as apports of the activity of a regular remodelling, in spatial and temporal fact during development and organ remodelling, in spatial and temporal or distinguishing between newly formed and pre-existing structures, e.g. membrane junctions and extracellular matrix components. The fluorescent contains may further be used to investigations where photobleaching techniques are employed, as detectable labels, as selectable markers, as blosensors in prokaryotic and eukaryotic cells, in protease cleavage assays, and as second messenger detectors. The nucleic acids can be used to assays, and as second messenger detectors. The nucleic acids can be used to assays, and as second messenger detectors animals or site-specific gene configurations in cell lines. The protein are placed protein and plants or animals or site-specific gene configurations in cell lines. The protein dryps and as placed place and place 
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Disclosure; Fig 3; 89pp; English.

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New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking
                                                     Fluorescent timer protein, protein movement, translocation, trafficking, promoter activity, gene expression, transgenic plant, gene modification,
                                      Discosoma sp. non-aggregating mutant timer protein E5NA encoding cDNA.
                                                                                                                                   /product= "Mutant E5NA protein"
                                                                                                           Location/Qualifiers
1. .678
                                                                    protein age; mutant; E5NA; 88.
                                                                                                                                                                                   13-JUN-2001; 2001WO-US019097.
                                                                                                                                                                                                  14-JUN-2000; 2000US-0211607P
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                                                                                                                                                                                                                  (CLON-) CLONTECH LAB INC.
                                                                                                                                                                                                                                 Terskikh A;
                                                                                                                          /*tag=
                                                                                                                                                                                                                                                 2002-154595/20.
                                                                                                                                                                                                                                                        P-PSDB; AAE17542.
                                                                                                                                                    WO200196373-A2.
                                                                                      Discosoma sp.
                                                                                                                                                                                                                                                                                                 or stability.
                                                                                                                                                                                                                                 Fradkov AF,
                                                                                                                                                                   20-DEC-2001.
                                                                                              Synthetic.
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The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer proteins are useful in monitoring the activity of a prometer, determining the age of a protein, identifying an agent that modulates the activity of a prometer and in controling a population of cells comprising a fluorescent timer proteins. The fluorescent timer proteins are also useful for assessing gene expression during development of a multicellular organism or during cellular differentiation, in response to a drug or other inducer of promoter activity, monitoring intracellular protein movement or translocation, protein rafficking, or protein response to a drug or other inducer of promoter activity, as a reporter to serve as a read-out of promoter activity of a regular protein movement or translocation, apporting intracellular protein movement or translocation, aspects of the activity of a regulatory element, for determining cell aspects of the activity of a regulatory element, for determining cell aspects of the activity of a regulatory element, for determining cell distinguishing between newly forteins and accumulated proteins, and in distinguishing between newly formed and pre-existing structures, e.g. membrane junctions and extracellular matrix components. The fluorescent techniques are employed, as detectable labels, as selectable markers, as blocensors in prokaryotic and eukaryotic cells, in protease cleavage conditications in cell lines. The present sequence is a cDNA encoding confications in cell lines. The present sequence is a cDNA encoding confications in cell lines. The present sequence is a cDNA encoding confications in cell lines. The present sequence is a cDNA encoding confications in cell lines. The present sequence is a cDNA encoding confications in cell lines. The present sequence is a cDNA encoding confication drafts. The protein derived in the protein derived in the protein as decompleted in the protei

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New monomeric and dimeric Anthozoan fluorescent protein variants with
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ADL46207
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                                                                                                                                                                                      206 CCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCG 265
                                                                                                                                                                                                                                 62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                266 AGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGCGGCGCGTGGCGACCGTGACCC 325
                                                                                                                                        2 CCGACGTGCCAGGGAACTACCCGCTGGACAGCTCGGACAACACCCTACCTGTGCGCACCCC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting transcriptional activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Discosoma red fluorescent protein; DsRed; AB interface; AC interface; fluorescent protein variant; transcription induction detection; fluorescence energy resonance transfer; FRET; protein kinase; protein phosphatase; ion indicator; ds; mutant; fast T1.
                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                              122 GCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                          326 AGGACTCCTCCTGCAGGACGCTGCTTCATCTACAAGGTGAAGTTCA 373
                                              DB 6; Length 678;
G; 104 T; 0 U; 0 Other;
                                                                                       79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Discosoma red fluorescent protein variant fast T1 DNA.
                                           Score 41.6; DB
Pred. No. 0.44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 3; 67pp; English.
C; 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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24-MAY-2001; 2001US-00866538
                                         Query Match 23.5%;
Best Local Similarity 53.0%;
Matches 89; Conservative
BP; 145 A; 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC24128 standard; DNA; 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TSIE/) TSIEN R Y.
(CAMP/) CAMPBELL R E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-743764/70.
P-PSDB; ADC24129.
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Sequence 678
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localisation or trafficking of a polypeptide of interest. A polypeptide marker is useful as markers to identify the location and amount of a target protein produced, where the target protein is fused to the marker, as a complement to or alternative for the green fluorescent protein or its spectral variant, for detecting induction of transcriptions in or applications involving fluorescence energy resonance transfer (PRET), which detects events as the function of the movement of fluorescent donors and acceptors towards or away from each other, for making thorescent sensors for protein kinase and phosphatase activities or indicators for ions and molecules such as CG2+, ZG2+, for identifying the presence of a molecule in a sample, for identifying a specific interaction of a first and second molecule, for determining whether a sample contains an enzyme or for determining the pH of the sample. (I) is useful for identifying a region or condition that regulates the activity of an expression control sequence. This sequence encodes Discosoma red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds; gene; red fluorescent protein; DsRed; fluorescence; red wavelen oligomerization; tetramerization; immunoassay; hybridization assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 678 BP; 141 A; 225 C; 205 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "DsRed variant T1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.5%; Score 41.6; DB 10;
53.0%; Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fluorescent protein variant fast T1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL46207 standard; DNA; 678 BP.
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29-JUL-2002; 2002US-00209208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 53.0
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The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form terramers and where the variant displays detectable fluorescence of at least one red where the variant displays detectable are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 AGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGCGGCGCGTGGTGACCGTGACC
 reduced propensity to oligomerize, and encoding polynucleotides, useful
in molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fluorescent protein variant; transcription induction detection; fluorescence energy resonance transfer; FRBT; protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                   23.5%; Score 41.6; DB 11; Length 678; 53.0%; Pred. No. 0.44; ive 0; Mismatches 79; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 Aggacrecereceaegaegeerecricareraegaegreaagrica 373
                                                                                                                                                                                                                                                                                                                                                                 Sequence 678 BP; 141 A; 225 C; 205 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Discosoma wild-type red fluorescent protein DNA #2.
                                                                       Disclosure; SEQ ID NO 5; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein phosphatase; ion indicator; ds.
                                                                                                                                                                                                                                                                                                                               coding sequence for the variant T1.
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24-MAY-2001; 2001US-00866538
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Best Local Similarity 53.09
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(CAMP/) CAMPBELL R E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-743764/70.
                                     movement in cells.
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The invention describes a polymucleotide sequence (I) encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced Discosoma red fluorescent protein (DsRed) variant having a reduced compressive, comprising anino acide substitutions at the AB and/or AC interfaces of the wild-type DsRed sequence (S1) comprising 225 amino acide, given in the specification, where the substitutions result in reduced propensity of the DsRed variant to form tetramers. (I) is useful for detecting transcriptional activity by providing a host cells constining a vector which comprises (I) operatively linked to an expression control sequence, and an unit to assay the variant fluorescent protein produced by (VII), where variant fluorescent protein produced by (VII), where variant fluorescent fluorescence is indicative of transcriptional activity. A polynucleotide concalisation or trafficking of a polypeptide of interest. A polypeptide of a canget protein produced by (VII), where variant fluorescent protein or trafficking of a polypeptide of interest. A polypeptide of target protein produced, where the target protein and amount of a target protein produced, where the target protein of the marker, as a complement to or alternative for the green fluorescent protein or applications involving fluorescence energy resonance transfer (FRET), which detects events as the function of the movement of fluorescent sensors for protein kinase and phosphatese activities or indicators to ions and molecules and scool molecule, for identifying a specific contains an enzyme or for determining whether a complement of a first and second molecule, for determining whether a complement of interaction of a first and second molecule, for determining whether a presence of a molecule in a sample, for identifying a region or condition that regulates the activity of the sample. Colains and acceptors for determining whether replaced to the produce of an expression control sequence. This sequence represents a modified of control sensor of condition that reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 CCAAGGTGTACGTGAAGCACCCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCG 268
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Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds, gene; red fluorescent protein; DsRed; fluorescence; red wavelength; oligomerization; tetramerization; immunoassay; hybridization assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 681 BP; 146 A; 223 C; 205 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.44; 79;
                                                                                                    Disclosure; SEQ ID NO 9; 67pp; English.
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                                                     transcriptional activity.
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RESULT 12
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                                                                                                                                                                                                                                                             The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DeRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DeRed sequence, where the substitutions result in reduced propensity of the DSRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in melocular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed coding sequence with codons optimised for human expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 ccaaggreracereaagcacececeacarececeaeracaacaagaagaagacerereceeg 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
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fuced propensity to oligomerize, and encoding polynucleotides, useful
molecular biology, e.g. in immunoassays or in tracking protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 681 BP; 146 A; 223 C; 205 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41.6; DB Pred. No. 0.44; 0; Mismatches
                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 3; 166pp; English.
                                                                                                                    Baird GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL46225 standard; DNA; 681 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2003; 2003WO-US010879.
                          09-APR-2003; 2003WO-US010879
                                                   2002US-00121258
2002US-00209208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                  Campbell RE,
                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                             WPI; 2003-845265/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                               movement in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003086446-A1.
                                                   10-APR-2002;
29-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2003
                                                                                                                  Tsien RY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Discosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL46225;
                                                                                                                                                                        New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form terramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed coding sequence with codons optimised for human expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 Addoctrica Agrada de de contra de la contra del la contra de la contra de la contra de la contra del la contra del
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monomeric and dimeric Anthozoan fluorescent protein variants with reduced propensity to oligomerize, and encoding polynucleotides, useful in molecular biology, e.g. in immunoassays or in tracking protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccaaggigracgreadecacceeceacareceesacracaagaagcrereeree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anthozoa; drFP583; fluorescent protein; non-bioluminescent organism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 aggacrecerecaggacgerecricareracaaggreaagrica 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 681 BP; 146 A; 223 C; 205 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.44;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
23.5%; Score 41.6;
Best Local Similarity 53.0%; Pred. No. 0.4
Matches 89; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 23; 166pp; English
                                                                                                                                                                                                                                                          Baird GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA48743 standard; cDNA; 695 BP.
10-APR-2002; 2002US-00121258.
29-JUL-2002; 2002US-00209208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US029473.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fluorescent labeling; ss.
                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                          Tsien RY, Campbell RE,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-845265/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Discosoma sp; "red"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          movement in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200034326-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA48743;
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268

61

Novel nucleic acid encoding a rapidly maturing chromo- or fluorescent

mutant of a Cnidarian chromo. or fluorescent protein or its mutant, useful for applications involving chromo. or fluorescent proteins.

19-DEC-2001; 2001US-0341723P.

(UYCH-) UNIV CHICAGO

Glick B;

Bevis B,

PI; 2003-569236/53

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The processing a novel fluorescent protein (nFP) from Discosoma sp. "red".

CDNA encoding a novel fluorescent protein (nFP) from Discosoma sp. "red",

a non-bioluminescent species of the Class Anthozoa. The wild-type drFP58;

nucleotide sequence was altered to optimise the codons for expression of

the fluorescent protein in mammalian cells. Fluorescent proteins can be

used in fluorescent labeling, a useful tool for marking a protein cell

or organism of interest. Unlike other markers used in protein labeling,

such as beta-galactosidase and luciferase. Methods involving fluorescent

require an exogenous cofactor or substrate. Methods involving fluorescent

or organism are also less laborious and less difficult to control than the

traditional methods of fluorescent labeling, where a protein of interest

is purified and then covalently conjugated to a fluorophore derivative.

Novel fluorescent proteins isolated from species of the Class Anthozoa

can be used as markers for gene expression and protein localization.

Studies, and in fluorescence resonance energy transfer (FRET) reactions.

They may have improved properties and better suitability for larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAGGTGTACGTGAAGCACCCCGCCGACTACCCCGACTACAAGAAGCTGTCCTTCCCCG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cnidarian; fluorescence resonance energy transfer; FRET; wild-type DSRED;
mutant; mutein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drFP583 is a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    excitations compared to prior art fluorescent proteins such as green
                                                                                                                                                                                  Novel fluorescent protein from non-bioluminescent Discosoma sp. red.
useful for fluorescent labeling and as markers.
                                                                                  Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.5%; Score 41.6; DB 3; Length 695; 53.0%; Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 695 BP; 149 A; 228 C; 209 G; 109 T; 0 U; 0 Other;
                                                                                  Green G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79; Indels
                                                                                                                                                                                                                                                                                     present sequence is humanised drfP583 cDNA.
                                                                                  Matz MV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                Labas YA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant-type DaRED encoding sequence.
                                                                                                                                                                                                                                             Claim 6; Page 75-76; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN33980 standard; DNA; 704 BP
  99US-00418529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2002; 2002WO-US040539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                  Fradkov AF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89; Conservative
                                          (CLON-) CLONTECH LAB INC
                                                                                                                                            WPI; 2000-423381/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fluorescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Discosoma sp.
                                                                                  Lukyanoy SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-2004
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XX
AC ADN3
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AC ADN3
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KW CNIC
KW MULE
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KW MULE
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CNIC
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OS DISC
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PD 03-
PF 18-
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XX
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The present invention relates to nucleic acid that encodes a rapidly maturing chromo or fluorescent mutant of a Chidarian chromo- or fluorescent protein or its mutant. The protein is useful in applications involving nucleic acid encoding a chromo- or fluorescent protein and is involving nucleic acid encoding a chromo- or fluorescent protein and is useful for producing a chromo and/or fluorescent protein which involves growing the cell, whereby the protein is expressed, and isolating the protein substantially free of other proteins. The protein is useful in applications involving chromo- or fluorescent protein and is useful as primers, whichisation probes, etc. The expression cassetus are useful as coloring agents which are capable of imparting color or pigment to a secoloring agents which are capable of imparting color or pigment to a particular composition of matter e.g., animals and plants. The chromoproteins may also find use as labels in analyte detection assays, e.g. assays for biological analytes of increst and as selectable markers in recombinant DNA applications, e.g. the production of transgenic cells and organisms. The fluorescence resonance energy transfer (FRET) applications, as biosensors in prokaryotic and eukaryotic cells, in applications involving the automated screening of arrays of cells expressing fluorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reporting groups by using microscopic imaging and electronic analysis, as second messenger detectors, and in fluorescence activated cell sorting applications and as in vivo marker in animals. The fluorescent proteins also find use in protease cleavage assays. The proteins can also be used is assays to determine the phospholipid composition in biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is assays to determine the phospholipid composition in biological membranes and as a fluorescent timer. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 CCAAGGIGIACGIGAAGCACCCCGACAICCCCGACIACAAGAAGCIGICCIIICCCCG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 AGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGCGCGTGGTGACCGTGACCC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalian codon optimised Discosoma red fluorescent protein; Discosoma; red fluorescent protein; directed evolution; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian codon optimised Discosoma red fluorescent protein DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 704;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 704 BP; 145 A; 237 C; 212 G; 110 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutant-type DsRED encoding sequence.
                                                                                                                                                                                                                                                                           Claim 7; SEQ ID NO 3; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ22476 standard; DNA; 723
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Matches
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us-10-617-978-17_copy_73_249.rng

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The present invention describes an isolated biscosome red itudrescent protein (1) comprising a 241 residue amino acid sequence (see ABP56678, S1), with one or more point mutations at amino acid position N24, F125, (K164, or M1813. Also described: (1) a fusion protein comprising (1); (2) an isolated nucleic acid encoding (1); (3) a vector comprising (1); (2) are revolval cDNA expression library comprising the nucleic acid of (2); (4) a host cell comprising the nucleic acid of (2); or errorival cDNA expression library comprising the nucleic acid of (2), or encoding (1); and (6) methods of making a fluorescent variant. The Discosoma red fluorescent proteins are useful for functional screens as a reporter for gene transcription (e.g. as a fusion protein), for target characterisation and localisation of fusion proteins, or for scaffolds for protein and peptide libraries. The fluorescent proteins can also be used as selectable markers or reporter molecules for a variety of bioassays, including methods that use fluorescence activated cell sorting (FACS) as a selection mechanism. The method of directed protein. The interest of the containing improved variants of the fluorescent protein. The method of directed protein. The method of method of directed protein. The method of method of method of directed protein. The method of method o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Discosoma red fluorescent protein, useful for functional screens as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reporter for gene transcription, for target characterization and localization of fusion proteins, or for scaffolds for protein and peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 TGGCCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 AGGGCTTCAAGTGGGGGGGGGGGTGATGAACTTCGAGGACGGCGGGGGGTGGTGACCGTGACCC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variants of Discosoma red fluorescent protein have greatly improved brightness, expression, and/or folding kinetics as compared to wild type or a codon optimised variant. The present sequence encodes a mammalian codon optimised Discosoma red fluorescent protein, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes an isolated Discosoma red fluorescent
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product= "Mammalian codon optimised Discosoma red
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_except= (pos:616. .618,aa:His)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              fluorescent protein"
                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-2001; 2001US-0291871P.
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     gb.
Discosoma
                                                                                                       Synthetic
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The present invention describes a chimeric protein comprising at least one signal protein that has a trafficking signal targeting to a subcellular organelle and at least one proteolytic claevage site for a proteolytic steep to that: (a) the proteolytic site or a signal masking protein the chameric protein is constructed, so that: (a) the trafficking signals of all the signal protein are inactivated by linking contein is present in cytosol; (b) the trafficking signal of at least one signal protein is present in cytosol; (b) the trafficking signal of at least one by the protease, and as a result at least one fragment protein that includes the activated signal protein is labelled with at least one fragment protein that includes the activated signal protein is labelled with at least one fragment protein and (c) the chimeric protein is labelled with at least one fluorescent abole signal in the cell is altered depending on the cleavage fluorescent protein and the position and intensity distribution of the fluorescent protein and the position and intensity distribution of the cluorescent protein and the position and intensity distribution of the fluorescent protein and the colline all saltered depending on the cleavage conspiration and intensity distribution of the comprising the chimeric protein in a cell; (2) a cell transformed with the recembinant gene or vector; (3) analysing the activity of a protease that a protease inhibitors in vivo; (4) a vector comprising the nucleic acid comprising the chimeric protein for detecting a protease inside a cell or tissue; and (10) detecting a protease inside a cell or tissue; and (10) detecting a protease inside a cell or tissue; and (10) detecting a protease inside a cell or tissue; and (10) detecting a protease inside a cell or tissue; and (10) detecting a protease inside the cell or tissue; the present sequence concerns in an expensive the cell or tissue; the present sequence concerns in an expensive the cell or tissue; the present sequence concerns in the cell or tissue; th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric protein, useful for detecting protease inhibitors inside the cell or tissue.
                                                                                                                                                                                                                              ₫₿.
                                                                                                                                                           RFP:PS(NIa protease):AtOEP7:GFP fusion protein DNA SEQ ID NO:51.
                                                                                                                                                                                                         chimeric protein; signal protein; trafficking signal targeting; proteolytic cleavage site; protease; protease inhibitor; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 51; 214pp; English.
                     ADL18131 standard; DNA; 1638 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-2002; 2002WO-KR001515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-2001; 2001KR-00048123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AHRA-) AHRAM BIOSYSTEMS INC.
                                                                                                                                                                                                                                                                                                       Obacco vein mottling virus.
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
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                                                                                                                 06-MAY-2004
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                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                   ADL18131;
ADL1813
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Gaps

23.5%; Score 41.6; DB 10; Length 1638; llarity 53.0%; Pred. No. 0.48; Conservative 0; Mismatches 79; Indels 0;

Similarity

Query Match Local Matches

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Run δ

Sequence:

Database

No.

Result

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E 2 (bases 1 to 354)

S Li,W.-X., Zeng,X.-C. and Zu,S.-Y.

Direct Submission

Submitted (15-MAY-1999) Department of Virology and Molecular
Biology, Virology Institution of Wuhan University, Luojia Street,
Wuhan, Hubel 430072, P.R. China

B 1,W.-X., Zeng,X.-C. and Zu,S.-Y.

Direct Submission

Submitted (05-0CT-2004) Department of Virology and Molecular
Biology, Virology Institution of Wuhan University, Luojia Street,
Wuhan, Hubel 430072, P.R. China
Sequence update by submitter

On Oct 6, 2004 this sequence version replaced gi:30844240.
AY569779 Cloning v
AX663075 Semicar
                                          AX663075 Sequence
AY342347 Red H-Pel
AY342348 Red H-Sti
AY490568 UAS-Red BX AY569780 Cloning v
AX5640435 Bordetell
BX640435 Bordetell
BX640419 Bordetell
AY488136 Zea mays
AL939110 Streptomy
AR180619 Sequence
AR136764 Sequence
AR136764 Sequence
AR336772 Sequence
AX330730 Sequence
AX33033 Sequence
AX33035 Sequence
AX33035 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae; Mesobuthus.

1 (bases 1 to 354)
2eng; X.-C., Li, W.-X. and Zu, S.-Y.
A novel cDNA sequence encoding the precursor of a new type of insect beta-neurotoxin, BmKBT from Chinese scorpion Buthus martensii Karsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF151798 354 bp mRNA linear INV 06-OCT-;
Mesobuthus martensii insect beta-neurotoxin (bt) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xrefe="axon:31649"
/tisbue_type="venom gland"
/note="authority: Buthus martensii Karsch"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .354
/organism="Mesobuthus martensii"
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Mesobuthus martensii
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                                                            AY342347
AY342348
AY342348
AY569780
AX122759
BX640435
BX640419
AY488136
SCO939110
AF236019
AR009714
AR136764
AR506027
SCO939104
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AX330939
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AF151798.2 GI:53828929
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/gene="bt"
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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INV 06-OCT-2004

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ENEYCRKICKLHGVTYGYCYNSRCWCEKLEDKDVTI"
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Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Mesobuthus.
I (bases 1 to 469)
Jiang, D., Cao, Z. and Li, W.
Cloning and characterizing of a new scorpion toxin from Buthus
                                                                                                                                                                                                                                                           GACGACGATCCAGGAAATTATCCGACAAATGCTTACGGTAACAAATATTATTGTACGATT 137
                                                                                                                                                                                                                                                                                            61 CTGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTAC 120
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Jiang,D., Cao,Z. and Li,W.
Direct Submission
Submitted (23-AFR-2003) Biotechnology, College of Life Sciences, Luojia Mountain, Wuhan, Hubei 430072, China
Location/Qualifiers
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                                                                                                                                                       Length 354;
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Pred. No. 3.9;
0; Mismatches 82; Indels
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                                                                                                                                                  th 25.9%; Score 45.8; DB 3; Similarity 53.7%; Pred. No. 4.1; 95; Conservative 0; Mismatches 82;
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329. .334
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note="BmKBT2'
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Direct Submitted (19-4MR-2002) Director-General of Biotechnology Center, Submitted (129-4MR-2002) Director-General of Biotechnology Center; National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishhara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:blo@mise.go.jp, WEL:http://www.bio.nite.go.jp/. Tel:81-3-3481-1933, Fax:81-3-3481-8424)
This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osonoe(*4), Norihiro Kushida(*4), Hidekazu Nakazawa(*4), Tomomi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7)
and Sacoshi Omura(*1,*3).
Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.
*I Kitasato Institute of Infectious Diseases
*3 The Kitasato Institute of Technology and Evaluation
*5 School of Science, Kitasato University
*4 National Institute of Technology and Evaluation
*5 School of Science, Kitasato University of Tokyo
*7 RIKEN, Genomic Sciences Center
*7 RIKEN, Genomic Sciences Center
*7 RIKEN, Genomic Sciences Center
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** Location/Qualifiers
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Complete genome sequence and comparative analysis of the industrial microcorganism Streptomyces avermitilis
Nat. Biotechnol. 21 (5), 526-531 (2003)
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                                                                                                               104 GACGACGATCCAGGAAATTATCCGACAAATGCTTACGGTAACAAATATTATTGTACGATT 163
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121 TGCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCAAGGTGTGA 177
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Streptomyces avermitilis genomic DNA, complete genome, section
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Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T., Kushida, N., Director-General of Biotechnology Center, Shiba, T. Bakaki, Y. and Hattori, M.
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Streptomyces avermitilis MA-4680
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
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KONNSAVA"
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/note="SAV5449"
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8039. .8719
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/gene="clpX2"
8880. .10166
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                                                                                                                                                                                                                                     7269. .7928
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Matches 72; Conservative
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YPLGODPSDLSGWQDFERLWRHLKGA"
complement(1655. .2782)
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TILITVLCTPPVQRIFFRFAMEPKMBMAFKRDATEIARBRAKA"
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                                                                                                                    strain: ATCC 31267,
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NCIMB 12804 or NRRL 8165.~synonym: Streptomyces
avermectinius"
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|mol_type="genomic DNA"
|strain="MA-4680"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="codon recognized: GGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (4060. .4133)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="tRNA-Glv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="tRNA-Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/note="SAV5445"
                                                                                                                                                                                                                            note="SAV5443"
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/gene="trn22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="trn39"
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gene="trn22"
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/gene="tig"
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'gene="tig"
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Non aggregating fluorescent proteins and methods for using the same Patent: WO 02068459-A 13 06-SEP-2002; Location/Qualifiers
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                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
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Centruroides limpidus limpidus sodium-channel modifier toxin Cll6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-MAR-2002) Bioestructura y Reconocimiento Molecular, Instituto de Biotecnologia, Av. Universidad 2001, Cuernavaca, Morelos 62210, Mexico Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                        1 (base; 1 to 316)
Corona, M. and Possani, L.D.
Corona, M. and Possani, L.D.
Impidus, that recognize Na(+)-channels
2 (bases i to 316)
Corona, M. and Possani, L.D.
Direct Submission
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/note="encodes sodium-channel modifier toxin Cl16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 AGAAGCACGCCTCGACTACGCCTACTGCTACGCGTTCCAGTGTTGGTGCGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proprotein"
62. .253
/product="sodium-channel modifier toxin Cll6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41.6; DB 3; Length 316;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .316
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/aub_species="limpidus"
/db_xref="taxon:29941"
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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synthetic construct
other sequences; artificial sequences.
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                                                                                                                                    Centruroides limpidus limpidus
Centruroides limpidus limpidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="preproprotein"
                           precursor, mRNA, complete cds
                                                                                AF491132.1 GI:31376359
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Best Local Similarity 60.7%;
Matches 68; Conservative
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misc_feature
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                              CCTGTGCGCACCCCTGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGT 107
                                                                                                                                    CGACTACGGCTACTGCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 CCCGCTGGACAGCTCGGACAACACCTACCTGTGCGCACCCCTGGGCGACAACCCGGACTG
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Pred. No. 6.8;
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                                                                                                /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="variant of sequence from Discosoma sp.
                                                                                                                                                                                                                               6; Length 678;
  Fluorescent timer proteins and methods for their use Patent: WO 0196373-A 3 20-DEC-2001; Clontech Laboratories Inc. (US)
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Sequence 7 from Patent W002068459.
AX824725
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/db_xref="taxon:32630"
/note="variant of sequence from Discosoma sp."
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                                                                                   6; Length 675;
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Fluorescent timer proteins and methods for their use Patent: WO 0195173-A 1 20-DEC-2001;
Clontech Laboratories Inc. (US)
Location/Qualifiers
                                                                             ch 23.5%; Score 41.6; DB 6; Length 6
1 Similarity 53.0%; Pred. No. 32;
89; Conservative 0; Mismatches 79; Indels
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/db_xref="taxon:32630"
/note="non-aggregating mutant"
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TITLE

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Directed evolution of protein in mammalian cells
Patent: US 6723537-A 1 20-APR-2004;
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Best Local Similarity 53.0%; Pred. No. 30;
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Patent: WO 02060941-A 7 08-AUG-2002;
Anticancer, Inc. (US)
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/organism="unidentified"
/mol type="unassigned DNA"
/db_xref="taxon:32644"
/note="Coral"
                        ARS27331
Sequence 1 from patent US 6723537.
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AX666133
AX666133.1 GI:29290961
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Corallimorpharia, Discosomatidae, Discosoma.
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|mol_type="unassigned DNA"
|db xref="taxon:32630"
|noTe="non-aggregating mutant"
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/organism="Discosoma sp."
/mol_type="unassigned DNA"
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/mol_type="taxon:32630"
/note="becription de la s quence artificielle : s quence de fusion"
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614 AGGACTCCTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCA · 661
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Sequence 3 from Patent WO2004083445.
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/note="Description de la s quence artificielle : s quence de fusion"
                                                                                                                                                                                                                                                                                                        62 TGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTACT 121
                                                                                                                                                                                                         61
                                                                                                                                                                                                         Gaps
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              2420 AGGACTCCTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCA 2467
                                                                                                                                                                                                                                                                                                                                                                                                            122 GCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                      DB 6; Length 2772,
                                                                                                                                                        79; Indels
                                                                                                      Score 41.6; DB
Pred. No. 27;
0; Mismatches
                                                                                                   Query Match 23.5%;
Best Local Similarity 53.0%;
Matches 89; Conservative
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model Run on:

July 30, 2005, 18:20:14; Search time 389.677 Seconds (without alignments) 2973.108 Million cell updates/sec

US-10-617-978-14_COPY_62_240 Title: Perfect score:

1 cggctgacgtcccgggaaac.......159 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

7287783 segs, 3236178273 residues Searched:

Total number of hits satisfying chosen parameters:

14575566

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/BCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
23: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
25: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
26: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
27: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
28: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
29: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
23: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
25: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
26: /cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df				•
Result No.	Score		Query Match Length DB ID	DB	ID	Description
-	38	21.2	:	21		Sequence 79, Appl
8	38	21.2		21		77.
m	36.8	20.6	195	21	US-10-721-793-139	139,
4	36.8	20.6		21	US-10-721-793-143	Sequence 143, App
Ŋ	36.8	20.6		21	US-10-721-793-147	147,
y	36.8	20.6		21	US-10-721-793-167	.67,
7	36.8	20.6		21	US-10-721-793-171	Sequence 171, App

App	App	App	App	App	App	App	App	App	App	Appl	Appl	App	App	Appl	Appl	App	Appl	Appl	App	ppli	ppli	Appl	Appl	Appl	Appl	ppli	ppli	Appl	Appl	Appl	Appl	Appl	Appl	App	App	App
155,	163,	153,	137,	141,	145,	Ľ.	161,	'n	ò			'n	'n		_				10	'n	7	27		25,				23,								
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
US-10-721-793-155	-10-721-793-16	-10-721-793-15	-10-721-793-13	-10-721-793-14	-10-721-793-14	-10-721-79	-10-721-793-16	-10-721-793-16	10-721-7	-10-721-793-1	10-721-793-1	-10-721-793-1	-10-721-793-17	-10-721-793-3	-10-721-	-10-721-793-1	-10-721-793-4	-10-721-79	-10-721-793-1	-10-721-793-	US-10-721-793-7	-10-721-793-2	-10-721-793-3	-10-721-7	-10-721-793-3	-10-721-793-	-10-721-793-	-10-721-793-2	-10-721-79	-10-721-793-1	-10-721-793-1	-10-721-793-2	US-10-721-793-21	-10-721-793-18	-10-7	
21	15	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
198	198	319	323	323	323	323	323	323	323	219	273	198	323	189	189	189	252	254	311	195	195	195	195	261	261	299	317	195	195	204	261	261	314	189	314	192
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ALIGNMENTS

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Sequence 79, Application US/10721793

Sequence 79, Application US/10721793

Sequence 79, Application No. US20050065331A1

GENERAL INFORMATION:

APPLICANT: Corrora Villegas, Miguel

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Garcia Briones, Georgina

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: Gracia Briones, Georgina

TITLE OF INVENTION: Venom of Scorpions of the Generation of Antivenoms to the

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

FILE REFERENCE: 2099.007001

CURRENT APPLICATION NUMBER: US 60/430,067

PRIOR FILING DATE: 2002-11-26

PRIOR PILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 294

SOFTWARE: Patentin Version 3.1

SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
1 LOCATION: (1)...(189)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Centruroides limpidus
```

Query Match

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JEBUICANT: Corona Villegas, Miguel
APPLICANT: Corona Villegas, Maguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Briones, Georgina
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION NUMBER: US/10/721,793
CURRENT APPLICATION NUMBER: US 60/430,067
PRIOR PRIOR DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE PATENTIN VENTION 3.1
SEQ ID NO 139
LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
CURRENT APPLICATION NUMBER: US/10/721,793
CURRENT FILING DATE: 2003-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Centruroides sculpturatus
FEATURE:
FEATURE:
LOCATION: (1)..(195)
OTHER INFORMATION:
PUBLICATION HORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 AGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTGAATTTCTGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 143, Application US/10721793
Publication No. USZ0050065331A1
GENERAL INFORMATION:
APPLICANT: Corona Villegas, Miguel
                                                                              Sequence 139, Application US/10721793
Publication No. US20050065331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: Toxicon
VOLUME: 39
ISSUE: 12
PAGES: 1893-1898
DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 AGGA 160
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OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Baiones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Rossani Postay, Lourival Domingos
TITLE OF INVENTION: Vecombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Vecombinant Immunogens for the Generation of Antivenoms to the
FILE REFERENCE: 2099.0070001
CURRENT APPLICATION NUMBER: US 10/721,793
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/430,067
NUMBER OF SEQ ID NOS: 294
SEQ ID NOS: 294
SEQ ID NO 77
                                                                                                                  48 TACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 TACATITIGCIGGAAATIGGGAGAACAAATACIGCATIGAIGAATGIAAAGAGAIAGGA 160
                                                                                                                                                      Gaps
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21.2%; Score 38; DB 21; Length 189; 60.8%; Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.2%; Score 38; DB 21; Length 31 Best Local Similarity 60.8%; Pred. No. 0.004; Matches 62; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat peptide
LOCATION: (62)..()
OTHER INFORMATION: Product= Sodium-channel modifier toxin
                                                         40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGAA 149
                                                                                                                                                                                                                                 108 GIGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTGAA 149
                                                                                                                                                                                                                                                                        161 ścreśriak cerariecia karacieri i reczenia do 202
                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Centruroides limpidus
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 77, Application US/10721793; Publication No. US20050065331A1; GENERAL INFORMATION:
                                                         62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (263)..(316)
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                        Best_Local Similarity
Matches 62; Conserv
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; OTHER INFORMATION:
US-10-721-793-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: 5'UTR
LOCATION: (1)..(4)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: 3'UTR
LOCATION: (263).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-10-721-793-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 316
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Sequence 167, Application US/10721793
Publication No. US20050065331A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corona Villegas, Miguel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL: Toxicon
VOLUME: 39
ISSUE: 12
PAGES: 1893-1898
DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(195)
                                                                                                   Query Match 20.6%;
Best Local Similarity 73.4%;
Matches 47; Conservative (
  ; DATABASE ENTRY DATE:
; RELEVANT RESIDUES: (1)..(195)
US-10-721-793-147
                                                                                                                                                                                                                                                                                                    157 AGGA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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Sequence 147, Application No. US20050065331A1

GENERAL INFORMATION:

APPLICANT: Corona Villegas, Miguel

APPLICANT: Corona Villegas, Miguel

APPLICANT: Garcia Rodriguez, Ma Consuelo

FILE REFERENCE: 2099.0070001

CURRENT APPLICATION NUMBER: US/10/721,793

CURRENT APPLICATION NUMBER: US 60/430,067

PRIOR FILING DATE: 2002-11-02

NUMBER OF SEQ ID NOS: 294

SEQ ID NO 147

BENCH: 195

MANDER DATE: 195

MANDER DATE: 195
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LOCATION: (1)..(195)
LOCATION: (1)..(195)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
JTTLE: that recognize Na+-channels
JOURNAL: Toxicon
                                                                                                                                                                                               LOCATION: (1)...(195)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Centruroides sculpturatus
                                                                                                     TYPE: DNA ORGANISM: Centruroides sculpturatus
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 143
                                                                                                                                                                                                                                                                                                                                                                                                ISSUE: 12
PAGES: 1893-1898
DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(195)
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PAGES: 1893-1898
DATE: 2001-12-01
                                                                                                                                                                                                                                                                                                                                                     Toxicon
                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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US-10-721-793-147
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APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Norma Adriana
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
FILE REPERENCE: 2009-0070001
CURRENT FILING DATE: 2003-11-26
PRIOR PLING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 167
LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D. TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing, IITLE: that recognize Na+-channels
                                                                                                                                     GTGAATTTCTGA 156
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                                                                                                                                                                                              95 AGAACCAAGGAGGTAGTTACGGGTATTGCTACGCTTTCGCATGCTGCTGCGAAGGTTTGC 154
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                                                                         Gaps
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   Length 195;
                                                                      17; Indels
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OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
                                                                                                                                     97 AGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Score 36.8; DB 21;
Pred. No. 0.0091;
0; Mismatches 17;
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APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Redriguez, Ma Consuelo
APPLICANT: Garcia Redriguez, Ma Consuelo
APPLICANT: Garcia Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
FILE REPERENCE: 2099.0070001
CURRENT APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 294
SEQ ID NOS: 294
SEQ ID NO 159
LENGTH: 198
                           TYPE: DNA
ORGANISM: Centruroides sculpturatus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(198)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
TITLE: Cancona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: Toxicon
VOLUME: 39
ISSUE: 12
PAGES: 1893-1898
BATE: 2001-12-01
BATEMASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(198)
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TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: Toxicon
VOLUME: 39
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LOCATION: (1)..(198)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.6%; Score 36.8; DB 21; Best Local Similarity 73.4%; Pred. No. 0.0092; Matches 47; Conservative 0; Mismatches 17;
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ORGANIGM: Centruroides sculpturatus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 159, Application US/10721793
Publication No. US20050055331A1
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DATABASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(198)
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; Sequence 155, Application US/10721793
; Publication No. US20050065331A1
; General INFORMATION:
; APPLICANT: Corona Villegas, Miguel
; APPLICANT: Corona Villegas, Miguel
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Gurzola Briones, Georgina
; APPLICANT: Becerril Lujan, Baltazar
; APPLICANT: Becerril Lujan, Baltazar
; APPLICANT: Possani Postay, Lourival Domingos
; TITLE OF INVENTION: Recombinant Immunogens for the Genus Centruroides
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TILE REFERENCE: 2099.0070001
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/430,067
; PRIOR PELING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 294
; SEQ ID NO 155
                                                                                                         APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Ourrola Briones, Georgina
APPLICANT: Becerial Lujan, Baltazar
APPLICANT: Becerial Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
FILE REPERBNCE: 2009.0070001
CURRENT FILING DATE: 2009.107001
CURRENT PILING DATE: 2003-11-26
PRIOR PILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 171
LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 AGAACCAAGGAGGTAGTTACGGGTATTGCTACGCTTTCGCATGCTGCGAAGGTTTGC 154
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Sequence 171, Application US/10721793
Publication No. US20050065331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Centruroides sculpturatus
                                                                                       APPLICANT: Corona Villegas, Miguel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(195)
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Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .. (195)
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PAGES: 1893-1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL: Toxicon
VOLUME: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-10-721-793-155
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LOCATION: (1)
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APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Redriguez, Ma Conauelo
APPLICANT: Garcia Redriguez, Ma Conauelo
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Usidez Cruz, Norma Adriana
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Deseani Postay, Lourival Domingos
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Venom of Scorpions for the Generation of Antivenoms
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
TITLE REPERENCE: 2099-0070001
CURRENT APPLICATION NUMBER: US/10/721,793
FRIOR APPLICATION NUMBER: US 60/430,067
FRIOR PRING DATE: 2002-12-02
SOFTWARE: PatentIn version 3.1
SEQ ID NO 153
LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(261)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last 2 basic aminoacids are cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1) (57)
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Centruroides sculpturatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE: 12
PAGES: 1893-1898
DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: mat_peptide
LOCATION: (58)..()
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: 819_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: 3'UTR
LOCATION: (265).
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NAME/KEY: CDS
LOCATION: (1).
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 163, Application US/10721793
; Sequence 163, Application US/10721793
; Publication No. US2005065331A1
; GENERAL INPORMATION:
    GENERAL INPORMATION:
    APPLICANT: Corona Villegas, Miguel
; APPLICANT: Garcia Redriguez, Ma Consuelo
; APPLICANT: Valdez Cruz, Norma Adriana
; APPLICANT: Usines, Georgina
    APPLICANT: Dessani Postay, Lourival Domingos
; TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; TITLE OF INVENTION NUMBER: US/10/721,793
; CURRENT APPLICATION NUMBER: US 60/430,067
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 294
; SEQ ID NO 163
; LENGTH: 198
; LENGTH: 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D. TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing, TITLE: that recognize Na+-channels
JOURNAL: Toxicon
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                                                                                                                                            97 AGAAACACGGIGIGGATIACGGGIAIIGCIACGCCTICCAAIGCIGGIGIGAAITICIGA 156
                                                                                                                                                                          95 AGAACCAAGGAGGTAGTTACGGGTATTGCTACGCTTTCGCATGCTGCGAAGGTTTGC 154
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                                 Query Match 20.6%; Score 36.8; DB 21; Length 198; Best Local Similarity 73.4%; Pred. No. 0.0092; Matches 47; Conservative 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
COCATION: (1). (198)
OTHER INFORMATION: Product= Sodium-channel modifier toxin
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGG
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US-10-721-793-153
IS-10-721-793-153
Publication US/10721793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Centruroides sculpturatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (1)..(198)
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PAGES: 1893-1898
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-10-721-793-163
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Length 319; Indels ဖ

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LOCATION: (5)..(265)
OTHER INFORMATION: Forduct= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 145, Application US/10721793

Sequence 145, Application US/10721793

Sequence 145, Application US/20050065331A1

SENERAL INFORMATION:
APPLICANT: Corona Villegas, Miguel
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Valdez Cruz, Norma Adriana
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baleaar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JONENNL: Toxicon
VOLUME: 39
ISSUE: 12
PAGES: 1893-1898
DATE: 2001-12-01
DATABASE ENTRY DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                    TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 323;
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20.6%; Score 36.8; DB 21;
Best Local Similarity 73.4%; Pred. No. 0.011;
Matches 47; Conservative 0; Mismatches 17;
                            FILE REFERENCE: 2099.007001
CURRENT APPLICATION NUMBER: US/10/721,793
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 141
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Centruroides sculpturatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES: (5)..(265)
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OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .. (323)
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NAME/KEY: mat_peptide
LOCATION: (62)..()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: sig_peptide
LOCATION: (5)..(61)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: 5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (5)..(265)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides FILE REPERENCE: 2099.0070001 US. 1070001 US. 1070001 US. 107001 US. 107001 US. 107001 US. 107001 US. 107001 US. 107001 US. 10700                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 141, Application US/10721793

Publication No. US2005005531A1

GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Garcia Briones, Georgina

APPLICANT: Garcia Briones, Georgina

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: Possani Postay, Lourival Domingos

APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
TITLE: that recognize Na+-channels
JOURNAL: Toxicon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat peptide
LOCATION: (62)..()
OTHER INFORMATION: Product= Sodium-channel modifier toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Centruroides sculpturatus
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ISSUE: 12
PAGES: 1893-1898
DATE: 2001-12-01
DATABASE ENTRY DATE:
RELEVANT RESIDUES: (5)..(265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (269)..(323)
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: 3'UTR
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US-10-721-793-141
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LOCATION: (5)..(265)
OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last 2 basic aminoacids are cut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Product= Sodium-channel modifier toxin PUBLICATION INFORMATION: Addition in Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing, TITLE: that recognize Na+-channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 AGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGAATTTTCTGA 156
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     CURRENT APPLICATION NUMBER: US/10/721,793
                CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SEQ ID NO 157
LENGTH: 323
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Job time : 390.677 secs
                                                                                                                                                                                                              TYPE: DNA ORGANISM: Centruroides sculpturatus
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RELEVANT RESIDUES: (5)..(265)
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (269)..(323)
OTHER INFORMATION:
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LOCATION: (5)..(61)
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LOCATION: (62)..()
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OTHER INFORMATION:
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PAGES: 1893-1898
DATE: 2001-12-01
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VOLUME: 39
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LOCATION: (269).
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                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
OTHER INFORMATION: and the last 2 basic aminoacids are cut
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APPLICANT: Corona Villegas, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Cruz, Norma Adriana
APPLICANT: Gurrola Briones, Georgina
APPLICANT: Becerril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
FILE REFERENCE: 2099.0070001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
ITILE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
JUURNEL: that recognize Na+-channels
JOURNAL: Toxicon
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OTHER INFORMATION: Product= Sodium-channel modifier toxin
                     CURRENT APPLICATION NUMBER: US/10/721,793
CURRENT FILING DATE: 2003-11-26
PRIOR PILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 145
LENGTH: 323
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Publication No. US20050065331A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Centruroides sculpturatus
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DATABASE ENTRY DATE:
RELEVANT RESIDUES: (5)..(265)
FILE REFERENCE: 2099.0070001
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LOCATION: (5)..(61)
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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PAGES: 1893-1898
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Length 323; Indels This Page Blank (uspto)

Sequence 1344, Ap Sequence 15, Appl Sequence 15, Appl Sequence 44, Appl Sequence 1071, Ap Sequence 12813, Ap Sequence 12813, A Sequence 14027, A Sequence 3, Appli Sequence 3, Appli

Sequence 52321, A Sequence 69, Appl Sequence 69, Appl

Sequence (

Sequence

Sequence 1, Appli Sequence 4380, Ap

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67 GAGATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGTGTGGGATTACGGGTATTGCT
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                            Sequence 32 Application US/09599632
Facent No. 6768002
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
TITLE OF INVENTION: SCORPION TOXINS
TITLE OF INVENTION: SCORPION
FILE REFERENCE: BB1375 US NA
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,410
PRIOR APPLICATION NUMBER: 60/140,410
PRIOR APPLICATION NUMBER: 60/140,410
PRIOR PILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Herman, Rafael
APPLICANT: Herman, Rafael
APPLICANT: Lee, Jian-Ming
TILLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1375 US NA
CURRENT APPLICATION NUMBER: US/09/599, 632
CURRENT APPLICATION NUMBER: 60/140,410
PRIOR PILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
LENGTH: 270
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Patent No. 6768002
GENERAL INFORMATION:
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; ORGANISM: Hottentotta judiaca
US-09-599-632-34
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310, Appl
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31107, Appl
3107, Appl
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1: /cgn2_6/ptodata1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata1/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata1/ina/PCTUS COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-599-632-32

US-09-599-632-36

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US-08-931-858E-97

US-08-931-858E-97

US-08-911-39-106

US-09-128-026-106

US-09-128-026-106

US-09-220-616-97

US-09-220-616-97

US-09-220-616-106

US-09-220-616-107

US-09-220-616-107

US-09-220-616-107

US-09-220-616-107

US-09-220-616-107

US-09-949-016-17157

US-09-949-016-17157

US-09-949-016-17157

US-09-948-016-17157

US-09-976-6594-3334

US-09-976-6594-3334
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Minimum DB E Maximum DB E

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Title: Perfect score:

Sequence:

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Run on:

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72 AATCCGGACTGCATTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 ACCTCGTGTTGGTGTATATTTGAAAAAAAAGAGACATCGATATTT 238
                                                                                                                                        Query Match 21.2%; Score 38; DB 4; Length 270; Best Local Similarity 56.0%; Pred. No. 0.00022; Matches 93; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MIBRANDT, JEFFREY D
APPLICANT: MIBRANDT, JEFFREY D
APPLICANT: LAMPE, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: LAMPE, PATRICIA A
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
MUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BOULEVARD, SUITE 1400
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Pred. No. 0.03;
0; Mismatches
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NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 9714
REFERENCE/DOCKET NUMBER: 9714
TELECOMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEPHONE: 314-727-6092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
                             ; ORGANISM: Hottentotta judiaca
US-09-599-632-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.6%;
Matches 71; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: ''...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-931-858E-97/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 Arcargarnarigregesacarrigraagracargeagreaarrargesiarrigrigge 190
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 rcaccrcererregrerejaararrigaaagaagagacarcaarri 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 CCTTCCAATGCTGGTGTGAATTTCTGAAGGATGAGAACGTGAAGGTCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 CCTTCCAATGCTGGTGTGAATTTCTGAAGGATGAGAACGTGAAGGTCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 TCACCTCGTGTTGGTGTGAATATTTGAAAGAAGAAGAAGACATCAATATTT 238
                                                                                                                                                                                                                                               22.8%; Score 40.8; DB 4; Length 270; 61.1%; Pred. No. 1.9e-05; tive 0; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 22.8%; Score 40.8; DB 4; Length 270; Similarity 61.1%; Pred. No. 1.9e-05; 66; Conservative 0; Mismatches 42; Indels
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Sequence 30, Application US/09599632

GENERAL INFORMATION:

APPLICANT: Herrman, Rafael

APPLICANT: Horny, James F.

APPLICANT: Hoe, Jiames F.

APPLICANT: Lee, Jiam-Ming

TITLE OF INVENTION: SCORPION TOXINS

FILE REFERENCE: BB1375 US NA

CURRENT APPLICATION NUMBER: US/09/599,632

CURRENT FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 60/140,410

PRIOR FILING DATE: 1999-06-22

NUMBER OF SEQ ID NOS: 38

SEQ ID NO 30

LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 3.5, Application US/09599632 | Patent No. 6768002 | GENERAL INFORMATION: APPLICANT: Herrman, Rafael APPLICANT: Herrman, James F. APPLICANT: Lee, Jian-Ming | TITLE REFERENCE: BB1375 US NA | CURRENT APPLICATION NUMBER: US/09/599,632 | CURRENT FILING DATE: 1999-06-22 | PRIOR FILING DATE: 1999-06-22 | NUMBER OF SEQ ID NOS: 38 | SEQ ID NO 36 |
                                                                                                   TYPE: DNA ORGANISM: Hottentotta judiaca
                                                                                                                                                                                                                                                                             Best Local Similarity 61.1%;
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Hottentotta judiaca
Microsoft Office
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US-09-599-632-30
                                                                                                                                                                         US-09-599-632-32
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                             SEQ ID NO 32
LENGTH: 270
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SOFTWARE:
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Matches

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285 CACCTGAGCCTITCAAAGGCTGCCTCTTGCTTGTGATTCTGAGAGACCAGGCTGGCCGCC 226

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25 CACTIGATICITICOGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCA

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285 caccricadecerrecadecrecererrecanteradades cadecadecrece 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 rrcasccaccacacacacacaces reces de contra de la contra de contr
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                                                                                                                                                                                                                                                   APPLICANT: JOHNSON JR., EUGENE M.
MILBRANDT, JEFFREY D.
KOTZBAUGR, PAUL T.
LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.2%; Score 32.6; DB 3; Length 336; 52.6%; Pred. No. 0.03; tive 0; Mismatches 64; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: PCT/US97/03461
FILING DATE: UNknown»
ATTORNEY AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 106:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
                                                                                            Sequence 106, Application US/08981739
Patent No. 6232449
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/09128026;
Patent No. 6403335;
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.;
APPLICANT: KOTZBAUER, PAUL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELEFAX: (314) 727-6092
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 71; Conserv
                                                          JS-08-981-739-106/c
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                                                          TTAAGATCTGTCAGAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 caccridadecritricada de crecitri de contrator de de desendades de contrator de 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.6; DB 3; Length 3
Pred. No. 0.03;
0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
CLASSIFICATION: <unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-981-739-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/08981739
Patent No. 6222449
GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILBRANDT, JEFFREY D.
KOTZBAUER, PAUL T.
LAMPE, PATRICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.2
Best Local Similarity 52.6
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -08-981-739-97/c
82
                                                                                                                                                                                                                 145
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OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: PCT//
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: HOLLAND, DONALD R.
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 7733 FOI CITY: ST. LOUIS STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63105-1817
                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-220-616-97/c
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Patent No. 6403335

GENERAL INFORMATION:
APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: MILBRANDT, JEFREY D.
APPLICANT: APPLICANT: APPRESENT A.
STRESPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STREET: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.2%; Score 32.6; DB 3; Length 336; 52.6%; Pred. No. 0.03;
APPLICANT: LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Indels
                                                                                                                                                                        COUNTRY: US

ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

RELICATION NUMBER: US/09/128,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
TELECOMUNICATION INFORMATION:
TELEPRAX: (314) 727-5188
TELEPRAX: (314) 727-5188
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
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Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-128-026-106/c
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285 caccricadecerrireaaggergeererrierreariergadagaecaggergeegee 226
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18.2%; Score 32.6; DB 3; Length 336;
Best Local Similarity 52.6%; Pred. No. 0.03;
Matches 71; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 91, Application US/09220616
Patent No. 6645937
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: MILBRANDT, JEFREY D.
APPLICANT: APPLICANT: PERSEPHIN T.
APPLICANT: APPLICANT: PERSEPHIN AND RELATED GROWTH FACTORS NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BOULEVARD, SUITE 1400
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 97616
TELECOMMUNICATION INFORMATION:
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-5188
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
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285 CACCTGAGCCTTTCAAAGGCTGCCTCTTGCTTGTGATTCTGAGAGACCAGGCTGGCCGCC 226
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                                                                                                                                                                                                                                      25 CACTTGAITCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGGACTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JOHNSON JR., EUGENE M.
MILBRANDT, JEFFREY D.
KOTZBAUBR, PAUL T.
LAMPE, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
                                                                                                                                        Score 32.6; DB 4; Length 336; Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4, Length 336;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/220,527
FILING DATE: 24-Dec-1998
CLIASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-AMG-1998
FILING DATE: 31-AMG-1998
FILING DATE: «Unknown>
                                                                                                                                                                                        64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.2%; Score 32.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97, Application US/09220527
Patent No. 6692043
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                           Query Match
Best Local Similarity 52.6%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          145 GTGAATTTCTGAAGG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 ĠGTCATCAAGGAAĠĠ 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ST. LOUIS
STATE: MISSOURI
  ; TYPE: nucleic acid
; STANNDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-220-616-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT, JEFFREY D.
APPLICANT: KOTZBAUGR, PAUL T.
APPLICANT: LAMPE, PERSEPHIN T.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: 7733 FORSYTH BOULEVARD, SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIE: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
APPLICATION NUMBER: PCT/US97/03461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 106, Application US/09220616 Patent No. 6645937 GENERAL INFORMATION:
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REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 97610
TELECOMMUNICATION INFORMATION:
TELEPAK: (314) 727-5188
TELEPAK: (314) 727-6092
INFORMATION FOR SEQ ID NO: 106: SEQUENCE CHARACTERISTICS:
REGISTRATION NUMBER: 35,197
REFRENCE/DOCKET NUMBER: 97616
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-5188
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 GTGAATTTCTGAAGG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCATCAAGGAAGG 151
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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STATE: MISSOURI
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-220-616-106/c
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                                                                                                                                                                                                                                                                                    US-09-220-616-97
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85 TTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGT 144
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             Sequence 97, Application US/09220407
Patent No. 6716600
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFRENCE/DOCKET NUMBER: 9714
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-692
TELEFAX: 314-727-692
                                                                                   145 GTGAATTTCTGAAGG 159
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nucleic acid
EDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                            JS-09-220-407-97/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 63105
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                                                                                                                                               85 TTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGT 144
                                                                                                                                                                                      TTCAGCCACCACACACCACAAGCTGCGGCTGAGAGCTGAGGCAGCTGCTGCCAATGGTGGT 166
                                                              CACTIGATICITCCGACAATACCIACCIGTGCGCCCCTTTGGGAGATAATCCGGACTGCA 84
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                         Gaps
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APPLICANT JOHNSON JR., EUGENE M.
KOTZBAUER, PAUL T.
LAMEP, PATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
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                       64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 63105-1817
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/220,527
FILING DATE: 24-Dec-1998
CLASSIFICATION: AUNTONN-
PRIOR APPLICATION DATA:
APPLICATION DATE: 31-Aug-1998
APPLICATION NUMBER: US/08/981,739
FILING DATE: 31-Aug-1998
APPLICATION NUMBER: PCT/US97/03461
FILING DATE: AUNTONN-
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 35,197
TELECOMMUNICATION INFORMATION:
  Pred. No. 0.03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-220-527-106
                                                                                                                                                                                                                                                                                                                                                   US-09-220-527-106/c
; Sequence 106, Application US/09220527
; Patent No. 6692943
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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52.6%;
                                                                                                                                                                                                                               145 GTGAATTTCTGAAGG 159
                                                                                                                                                                                                                                                                      165 GGTCATCAAGGAAGG 151
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Best Local Similarity 52.6
Matches 71; Conservative
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Best Local Similarity
Matches 71; Conserva
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225 irckieccaccackideckickideckiekidakiericadeckiekideckidakiderider 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBARNDT, JEFFREY D
APPLICANT: LAMPE, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: KLEIN, ROBERT
APPLICANT: TEAUNGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/220,407 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S: HOWELL & HAFERKAMP, L.C.
7733 FORSYTH BOULEVARD, SUITE 1400
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Search completed: July 30, 2005, 20:19:10 Job time : 87.4775 secs

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AGENCOURT BOGUO61TR BONRY58TF

fm83b12.y BONJE57TR

BX338057 AGENCOURT AGENCOURT

CH230-397 KD1925.p1 Forward s BOHCI74TF 331PvH05 BOGQY14TF odi95h04. BOHLM46TR

BH548329

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BN5175692

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AW343516 fi45a12.x1 Sugano Kawakami zebrafish DRA Danio rerio cDNA clone IMAGE:2640574 3' similar to SW:MCM2_XENLA P55861 DNA REPLICATION LICENSING FACTOR MCM2 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotes, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cyprinicames, Cyprinidae; Danio.

1 (Dases 1 to 414)
Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S., Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T., Martin, J., Pape, D., Steptoe, M., Underwood, K., Thaising, B., Ritter, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: S.L. Johnson
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Washington University Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami library constructed by Dr. Sumio                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev stage="adult"
/lab_host="DH10B (phage resistant)"
/clone lib="Sugano Kawakami zebrafish DRA"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); lst strand cDNA was primed
with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="raxon:7955"
/clone="livkGb:2646574"
/sex="mixed (one male and one female, including
unfertilized eggs)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .414
/organism="Danio rerio"
/mol_type="mRNA"
/strain="AB"
                                                          B1880995
BZ456120
CK027614
BH486210
BZ447705
BX338057
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CD253204
AL517987
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BZ175692
BZ302592
CR249625
BH578500
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Danio rerio
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AW343516.1 GI:6839882
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  RESULT 1
AW343516/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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1 cggctgacgtcccgggaaac.....atgagaacgtgaaggtctga 179
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Maximum Match 100%
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DNA

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(TGTTGGCCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACATGTG. XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments (1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTGCTCTAAAAGGTGCG and 3' end primer CGACCTGCAGGACAA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 AGCAGCTGGTTTCTGAGCAGGTCTCATATCAGCGCAACCGTTTGGGAGCCCAGCAGGACA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCATTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 CCATCGAGATCGCAGAGAAGACCTGGTGGACAAGGCTGACAAATCAACCATCCACAGCC 198
                                                                                                                                                                                                                                                                                                                                                                                                                      22 ACCCACTTGATTCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACT 81
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                          Query Match
19.6%; Score 35; DB 2; Length 414;
Best Local Similarity 54.2%; Pred. No. 1.3;
Matches 71; Conservative 0; Mismatches 60; Indels
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Washington University School of Medicine
Baal: submissions@watson.wustl.edu
Plate: lkh84 row: c column: 10
Seq primer: -21UPpOT forward
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
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High quality sequence stop: 551.
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BZ047564.1 GI:23644179
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BONHL22TR BO 1.6 2 KB tot Brassica oleracea genomic clone BONHL22, genomic survey sequence.
BZ506790.
BZ506790.1 GI:27028164
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                                  431 TTGCTTTTATAGAAATATGTTTCTGTTCGCCGCGTTCTTCCCTGATCAGGACGCCGCTC 490
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87
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                          CB803038
AMGNNUC:MRBE4-00005-A2-A rat brain E15 (10375) Rattus norvegicus
CDNA clone mrbe4-00005-a2 5', mRNA sequence.
 TIGATICITCCGACAATACCTACCTGTGCGCCCCTTTGGGGAGATAATCCGGACTGCATTA
                                                                        88 AGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTG
                                                                                                          491 ACAGCTGTTGCCGACACGGCGATGTACAAGAATAAAGGTTCCCCCTCCACGGGTTTTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .411
/organism="Rattus norvegicus"
/mol_type="mRN21016"
/db_xref="texon:1016"
/clone="mrbe4-00005-a2"
/tissue type="brain E15"
/clone_lib="rat brain E15"
/note="Vector: pBCB; Site_1: BstXI; Site_2: Not1; rat brain E15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GABACTACCCACTTGATTCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATC
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Plate: 00005 row: a column: 2.
Location/Qualifiers
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Pred. No. 3.2;
0; Mismatches
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Amgen EST Program.
Amgen Rat EST Program
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Best Local Similarity 51.7%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
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Gaps

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19.3%; Score 34.6; DB 8; Length 728; ilarity 55.4%; Pred. No. 2; Conservative 0; Mismatches 54; Indels

Best Local Similarity Matches 67; Conserv

Query Match

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Direct Submission Submission Submitted (123-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 26-JUL-1999
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides; Drosophilidae; Drosophila.
                                                                                                                     /organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TO1000DH3"
/db xref="Teaxon:3712"
/clone="BOGQH46"
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/db xref="texon.7227"
/clone="BACN09J03"
/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
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Pred. No. 3.9;
0; Mismatches
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BOGGH46TF BOGQ Brassica oleracea genomic clone BOGGH46, genomic survey sequence.
BH535763. GI:17767301
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Brassica oleracea
Brassica oleracea
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Brassica oleracea
Brassica, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 595)
1 (com.,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
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Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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/clone="BONHL22"
/clone=lib="B0_1.6_2_KB tot"
/note="Vector: pHO51; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHŌS1 using BstXI linkers"
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Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Frae Whole genome shotgun sequencing of Brassica oleracea Other GSSs: BOGQH46TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
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Pred. No. 3.6;
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/strain="TO1000DH3"
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Best Local Similarity 53.4%;
Matches 71; Conservative (
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Endantota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosids II, Barasicales; Brassicaceae; Brassica.

I (bases 1 to 580)

Statari, M., O'Shaughnessy, A., Palmer, L., Bahret, A., Baker, J., Balija, V., Cunnius, D.M., Katenberger, F., King, L., Kirchoff, K., Kuit, K., Miller, B., Muller, S., Nascimento, L., Preston, R., Santos, L., Shah, R., Zutavern, T., Dedhia, N., Rabinowicz, P.D. and McCombie, W.B.

Whole Genome Shotgun Reads from Brassica oleracia (2002b)

M. Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazon Genome Sequencing Center

Cold Spring Harbor Laboratory

Po Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8887

Email: mccombie@cebl.org

Plate: 9138 row: b column: 03

Seq primer: -21UnivRev

Class: shotgun

High quality sequence stop: 580.
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BH675875
BH675875.1 GI:18746318
                                580 bp DNA linear GSS 25-FEB-2002 gt38b03.g1 BoBuds01 Brassica oleracea genomic clone gt38b03 5', genomic survey sequence.
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18.4%; Score 33; DB 8; Length 580;
Best Local Similarity 54.5%; Pred. No. 6.6;
Matches 66; Conservative 0; Mismatches 55; Indels
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/organism="Brassica oleracea"
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/db_xref="taxon:3712"
/clone="gt38b03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Ambystoma tigrinum tigrinum"
/mol_type="mRNA"
/mol_type="mRNA"
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/db_xref="taxon:43116"
/fissue_type="Liver, Lung, Kidney, Heart, gonad, brain and gill tissues collected from metamorphosing larvae"
/clone_lib="AG"
                                                                                                                                                                                                                                                                                                                                                                       CN063005
Ag2_p39_024_M13R AG Ambystoma tigrinum tigrinum cDNA, mRNA
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                                                                                                                                89 GATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTGA 148
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                                   GGACTGCATTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCA 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The EST is quality trimmed at the ends with a 20 base window and quality threshold of 15 (phred quality score). Please visit http://salamander.uky.edu For any information(trace,quality files etc) regarding this EST.

Location/Qualifiers
       AAACTACCCACTIGATICITCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ambyatoma tigrinum tigrinum
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1092)
Putta,S., Smith,J.J., Walker,J.A., Rondet,M., Weisrock,D.,
Monaghan,J., Samuels,A.K., Kump,K., King,D.C., Maness,N.J.,
Habermann,B., Tanaka,E., Bryant,S.V., Gardiner,D.M., Parichy,D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                From biomedicine to natural history research: EST resources for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATTCTTCCGACAATACCTACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ambystoma tigrinum tigrinum (Eastern tiger salamander)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.5%; Score 33.2; DB 7; Length 1092; larity 51.3%; Pred. No. 6.7; Conservative 0; Mismatches 73; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biology
University of Kentucky
TH Worgan Building, Lexington, KY 40506, USA
Tel: 859 257 1988
Fax: 859 257 1717
Email: srvoss@uky.edu
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BMC Genomics 5 (1), 54 (2004)
Contact: SR Voss
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CN063005.1 GI:45839068
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nes 77; Conserv
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Matches
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BONLH48TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONLH48,
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Brassica oleracea
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 AGAICTGICAGAAACACGGIGIGGATIACGGGIAITGCIACGCCTICCAAIGCIGGIGIG 147
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/mol type="genomic DNA"
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/clone="BONLH48"
/clone="Borctor: pHoS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHōS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                         28 TIGATICTICCGACAATACCTACCIGIGCGCCCCTTIGGGAGATAATCCGGACTGCATTA
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                                                                                                  /mol_type="genomic DNA"
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/clone lib="BoGGJM34"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
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DNA is from a doubled haploid provided by Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Best Local Similarity 54.5%; Pred. No. 7.1;
Matches 66; Conservative 0; Mismatches 55; Indels
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Seg primer: TR
Class: sheared ends.
Location/Qualifiers
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/organism="Brassica_olexacea"
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Class: sheared ends.
Location/Qualifiers
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Matches 66; Conservative
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Fax: 301-838-0208
Email: cdtown@tig
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BOGJM34TR BOGJ Brassica oleracea genomic clone BOGJM34, genomic
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Warayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                   Brassica oleracea
Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Wagnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II, Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 644)

Tomn, C. D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other GSSs: BOGJM31F
Contact: Chris Town
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Fax: 301-838-0208
Email: cdrownedigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                      Tel: 301-838-3523
Fax: 301-838-0208
Email: cdcown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
Class: sheared ends.
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Pred. No. 6.8;
0; Mismatches 55; Indels
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Best Local Similarity 54.5%;
Matches 66; Conservative 0
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BH439076
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Aspergillus flavus

Aspergillus flavus

Bukaryota, Fugis, Ascomycota, Pezizomycotina, Eurotiomycetes,

Bukaryota, Fugis, Ascomycota, Pezizomycotina, Eurotiomycetes,

Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.

Entropy Mylicalaw, C.A., Nierman, W.C., Bhatnagar, D. and Cleveland, T.E.

Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops

L. FEMS Microbiol. Lett. (2004) In press

Contact: Yu J. and Research Unit

Food and Feed Safety Research Unit

Food and Feed Safety Research Unit

Food boot Te. Lee Boulevard, New Orleans, LA 70124, USA

Tel: 504 286 4405

Fax: 504 286 4419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increal Vector: pBlueScript (SK+) (Stratagene), antibiotic selection marker: Garbenicillin; Site 1: Not1, at the 5 prime end, Site_2: EcoRI, at the 3 prime end; This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jiuyu@errc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC (jiuyu@errc.ars.usda.gov) for clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CO141971
454 bp mRNA linear EST 17-JUN-2004
EST818642 Aspergillus flavus Normalized cDNA Expression Library
Aspergillus flavus cDNA clone NAFFH21 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="asexual mycelia"
/cell_type="mycelia"
/dev_grage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DHentb Ti resistant cells"
/clone_lib="Aspergillus flavus Normalized cDNA Expression
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/clone="NAFEJ04"
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/strain="NRRL 3357"
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                                                                                                                                                                        AGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTG 147
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                                                                                             Trigoritaria rada a a a a a control de contr
                                                                                                                                                                                                                                           223 ACAGCIGITGCCGACACGCGACGTACAAGAACAAAGGITTCCCCTCCACAGGITTTGCG 282
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Canis.
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1 (Bases 1 to 637)
2 (Chases 1 to 637)
3 Callueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H., Henrich, J. and Loebbert, R.
Dog arrayTAG CDNA clone collection
Unpublished (2004)
Contact: Thomas Schueter
LION bioscience AG
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/note="Organ: kidney; Vector: Dog pBluescript LION"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waldhoferstrasse 98, D-69123 Heidelberg, Germany Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas Schlueter@lionbioscience.com.
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/tissue_type="kidney"
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/lab_host="DH108"
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/strain="Beagle"
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                                                                                                                                                                                                                                                                                                                                 Email: jiuyu@srrc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC (jiuyu@srrc.ars.usda.gov) for clone
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                   Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes, Eurotiales, Trichocomaceae, Aspergillus. 1 (bases 1 to 454)
Yu.J., Whitelaw, C.A., Nierman, W.C., Bhatnagar, D. and Cleveland, T.E. Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops Contact: Yu J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jobber 1 Stratagene), antibiotic selection marker: Carbenicilin; Site 1: Not1, at the 5 prime end; Site 2: EcoR1, at the 3 prime end; Site 2: EcoR1, at the 3 prime end; This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different endium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="asexual mycelia"
/cell_type="mycelia"
/dev_stage="developmental stages from 18 to 96 hours"
/dev_stage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DH108 T1 resistant cells"
/clone_lib="Aspergillus flavus Normalized cDNA Expression
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                                                                                                                                                                                                            Food and Feed Safety Research Unit
USDA/ARS, Southern Regional Research Center
1100 Robert E. Lee Boulevard, New Orleans, LA 70124,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Aspergillus flavus"
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/strain="NRRL 3357"
/db_xref="taxon:5059"
/clone="NAFFH21"
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                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                            JOURNAL
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selection marker: Carbenicillin; Site 1: Not1, at the 5 prime end; Site 2: EcoRI, at the 3 prime end; This normalized cDNA expression library was constructed using a mixture of mycelial calls grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."
                                                                                                                                                                                                                                                                                                                                                            Email: jiuyu@srrc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC (jiuyu@srrc.ars.usda.gov) for clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
1 (bases 1 to 455)
                                                                 and Cleveland, T.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 AGAAACACGGTGTGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTGAATTTCTGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 Grerecercicacida partrececa a cerecerce e centra e contra en 160
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                               1 (bases 1 to 455), Vierman, W.C., Bhatnagar, D. and Cleveland, T. V.J., Whitelaw, C.A., Nierman, W.C., Bhatnagar, D. and Cleveland, T. Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops PEMS Microbiol. Lett. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ccerccacaaceccercaceccarrarccercaecaarecercaecarearerc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ecx="aesxual mycelia"
/cell type="mycelia"
/dev_stage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DH10B T1 resistant cells"
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                                                                                                                                                                                 Contact: Yu J
Food and Feed Safety Research Unit
USDA/ARS, Southern Regional Research Center
1100 Robert E. Lee Boulevard, New Orleans, LA 70124,
Far: 504 286 4405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Indels
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/organism="Aspergillus flavus"
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/clone="NAFAU67"
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Job time : 1968.96 secs
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/strain="NRRL 3357"
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                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Sequence 16, Appl Sequence 16, Appl Sequence 45, Appl Sequence 45, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1272, Appli Sequence 5166, Appli Seq

US-09-923-876-1272 0 US-09-923-876-1272 1 US-10-260-238-5616 8 US-10-425-114-13478 8 US-10-425-114-20725

ALIGNMENTS

APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-222
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEROID NO 5636
LENGTH: 2748 ; Sequence 5636, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION: ORGANISM: Streptomyces avermitilis ; LOCATION: (1)..(2748) US-10-156-761-5636 FEATURE: NAME/KEY: CDS TYPE: DNA Sequence 5636, Ap Appl Appl Appl Appl Appl Sequence 1, A Sequence 75, B Sequence 73, A Sequence 38, B Sequence 13, A Sequence 36, A Description

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Publication No. US20050065331A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Corona Villegas, Miguel
APPLICANT: Carcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Rodriguez, Ma Consuelo
APPLICANT: Garcia Briones, Georgina
APPLICANT: Georgina
APPLICANT: Beceril Lujan, Baltazar
APPLICANT: Possani Postay, Lourival Domingos
TITLE OF INVENTION: Venom of Scorpions of the Generation of Antivenoms to the
FILE REPERENCE: 2099,0070001
FILE REPERENCE: 2099,0070001
CURRENT APPLICATION NUMBER: US/10/721,793
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                                                                                                                         48 CCTGTGCGCACCCCTGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGT 107
                                                                                                                                                                                                                                                108 CGACTACGGCTACTGCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACG 166
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                                                                 0; Gaps
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Query Match

24.7%; Score 43.8; DB 15; Length 2748;
Best Local Similarity 60.5%; Pred. No. 0.0007;
Matches 72; Conservative 0; Mismatches 47; Indels 0;
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; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
PRIOR FILING DATE: 2001-06-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: (4187715)
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ses 72; Conserva
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LENGTH: 9025608
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HUDILGEATION NO. USZU050065331A1

GENERAL INFORMATION:

APPLICANT: Corona Villegas, Miguel

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Garcia Rodriguez, Ma Consuelo

APPLICANT: Garcia Briones, Georgiana

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: Becerril Lujan, Baltazar

APPLICANT: PRESARIN POSEAJ, Vocana de Scorpiona of the Genus Centruroides

ITILE OF INVENTION: Venom of Scorpiona of the Genus Centruroides

ITILE OF INVENTION: Venom of Scorpiona of the Genus Centruroides

ITILE OF INVENTION NUMBER: US/10/721,793

CURRENT FILING DATE: 2003-11-26

NUMBER OF SEQ ID NOS: 294

SOFTWARE: PATENTING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 294

SOFTWARE: PATENTING DATE: D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 CGGCTGCAAATACGGGTGCTATGAATTGGGTGACGATTACTGCGATAGGAAATGCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 CGGACAACACCTACCTGTGCGCACCCCTGGGCGACAACCCGGACTGCATCAAGATCTGCC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(192)
; OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.5%; Score 41.6; DB 21; Best Local Similarity 60.7%; Pred. No. 0.0026; Matches 68; Conservative 0; Mismatches 44;
                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Centruroides limpidus limpidus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Centruroides limpidus limpidus
PRIOR APPLICATION NUMBER: US 60/430,067
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 294
SCFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 73, Application US/10721793
; Publication No. US20050065331A1
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LOCATION: (62)..()
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LOCATION: (5)..(61)
OTHER INFORMATION:
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NAME/KEY: 3'UTR
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LOCATION: (5).
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ORGANISM: Discosoma species
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JAPPLICANT: Lukyanov, Sergey A

APPLICANT: Lukyanov, Arcady F.

APPLICANT: Labas, Yulii A.

APPLICANT: Tarakkov, Arcady F.

APPLICANT: Tarakkov, Arcady F.

APPLICANT: Terskikh, Alexey

TITLE OF INVENTION: No. US20020197676Alel Chromophores/Pluorophores and

TITLE OF INVENTION: No. US20020197676Alel Chromophores and

TITLE OF INVENTION WHERE: US/10/06,922

CURRENT PILING DATE: 209-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/458,477

PRIOR APPLICATION NUMBER: 09/457,556

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR PRILICATION NUMBER: 09/44338

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-11-19

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FESTSEQ FOR Windows Version 4.0
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                                                                                                                                                          35 CGGACAACACCTTACCTGTGCGCACCCCTGGGCGACAACCCGGACTGCATCTGCC 94
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                                                 Query Match 23.5%; Score 41.6; DB 21; Length 316; Best Local Similarity 60.7%; Pred. No. 0.0027; Matches 68; Conservative 0; Mismatches 44; Indels 0
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Pred. No. 0.003;
0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-10-006-922-38
US-10-006-922-38, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
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Sequence 13, Application US/10081864
Publication No. US20030022287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
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Best Local Similarity 53.0
Matches 89; Conservative
US-10-721-793-73
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APPLICANT: Yanushevich, Yuriy
APPLICANT: Savietky, Alexandr
APPLICANT: Savietky, Alexandr
APPLICANT: Savietky, Alexandr
APPLICANT: Pradkov, Arcady
TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: Methods for Using the Same
FILE REPERENCE: CLON-067
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT FILING DATE: 2002-06-19
PRIOR PRICATION NUMBER: 60/20093
PRIOR PRILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR PILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 675
TYPE: NUMBER 675
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APPLICANT: Lukyanov, Sergey A
APPLICANT: Lukyanov, Arcady F.
APPLICANT: Eabas, Yulii A.
APPLICANT: Fradkov, Arcady F.
APPLICANT: Habs, Yulii A.
APPLICANT: Perskikh, Alaxey
TITLE OF INVENTION: No. US20020197676Alel Chromophores and
TITLE OF INVENTION: NUMBER: 2011-12-04
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NOS: 46
SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.5%; Score 41.6; DB 14; Length 675; Best Local Similarity 53.0%; Pred. No. 0.003; Matches 89; Conservative 0; Mismatches 79; Indels 0
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US-10-081-864-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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TITLE OF INVENTION: No. US20030022287Al Aggregating Fluorescent Proteins and TITLE OF INVENTION: Methods for Using the Same FILE REFERENCE: CLON-067
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR PILING DATE: 2001-02-1
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASTESC for Windows Version 4.0
SEQ ID NO 14
LENGTH: 678
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Sequence 5, Application US/10121258

Publication No. US20030059835A1

GENERAL INFORMATION:

APPLICANT: Telan, Roger

APPLICANT: Campbell, Robert

TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT

TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME

FILE REPERENCE: UCO3.1CP2CP1

CURRENT APPLICATION NUMBER: US/10/121,258

CURRENT APPLICATION NUMBER: US/10/121,258

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: 09/794,308

PRIOR FILING DATE: 2001-02-26

SPRIOR FILING DATE: 2001-02-26

SPRIOR SEQ ID NOS: 78

SOFTWARE: FRREEEQ for Windows Version 4.0

LENGTH: 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 AGGACTCCTCCTGCAGGACGCTGCTTCATCTACAAGGTGAAGTTCA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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APPLICANT: Annushevich, Yuriy
APPLICANT: Savistky, Alexandr
APPLICANT: Savistky, Alexandr
APPLICANT: Savistky, Alexandr
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: NO. US2003002067
FULLS REPERBRICE: CLON.067
CURRENT APPLICATION NUMBER: 10/006,922
PRIOR FILING DATE: 2001-12-04
PRIOR FLING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 678
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                                                                                                                                                                                                                                                           206 ccaaggigtacgigaaggacacccccaacarccccaaciacaagaagcigiccirccccg 265
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                                                                                                                                                                                                  Gaps
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                                                                     Score 41.6; DB 13; Length 678;
Pred. No. 0.003;
0; Mismatches 79; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GCTACGCGTTCCAGTGTTGCTGCAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 AGGACTCCTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.5%; Score 41.6; DB 14; Length 678; 53.0%; Pred. No. 0.003; cive 0; Mismatches 79; Indels 0
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| Publication No. US20030022287A1
| GENERAL INFORMATION:
| APPLICANT: Lukyanov, Konstantin;
| APPLICANT: Lukyanov, Konstantin;
| APPLICANT: Sanushevich, Yuriy;
| APPLICANT: Savistky, Alexandr;
| APPLICANT: Fradkov, Arcady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-10-081-864-7
Sequence 7, Application US/10081864
Publication No. US20030022287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
                                                                         Query Match
23.5%;
Best Local Similarity 53.0%;
Matches 89; Conservative
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Best Local Similarity 53.0°
Matches 89; Conservative
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ORGANISM: Discosoma sp
US-10-081-864-7
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US-10-081-864-14
               US-10-006-922-36
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US-10-006-922-35
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  266 AGGCCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGGTGACCGTGACCC 325
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                                                122 GCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.5%; Score 41.6; DB 16; Length 678; Best Local Similarity 53.0%; Pred. No. 0.003; Matches 89; Conservative 0; Mismatches 79; Indels 0
                                                                                              326 AGGACTCCTCCCTGCAGGACGGCTCCTTCATCTACAAGGTGAAGTTCA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACGAGAACGTCA 169
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                                                                                                                                                                                                  Sequence 1, Application US/10315920
| Publication No. US20030175809A1
| GENERAL INFORMATION:
| APPLICANT: Frackov, Arcady Fedorovich
| APPLICANT: Frackov, Arcady Fedorovich
| TITLE OF INVENTION: FLOKESCENT TIMER PROTEINS AND METHODS
| TITLE OF INVENTION: FOR THEIR USE
| FILE REFERENCE: CLON-077CIP
| FILE APPLICATION NUMBER: 60/211,607
| PRIOR APPLICATION NUMBER: PC7/US01/19097
| PRIOR FILING DATE: 2001-06-14
| PRIOR FILING DATE: 2001-06-13
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 1
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FUBLICATION NO. US20030175809A1
FUBLICANT: FRACKO, Arcady Fedorovich
TITLE OF INVENTION: FLOORESCENT TIMER PROTEINS AND METHODS
TITLE OF INVENTION: FOR THEIR USE
FILE REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT APPLICATION NUMBER: 05/211,607
FRIOR APPLICATION NUMBER: 60/211,607
FRIOR APPLICATION NUMBER: PCT/US01/19097
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FARESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: variant of sequence from Discosoma sp
US-10-315-920-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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206 CCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCG 265
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                                                                                                                                                                                                            Length 678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 AGGACTCCTCCTGCAGGACGCTGCTTCATCTACAAGGTGAAGTTCA 373
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APPLICANT: Terekikh, Alexey
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
TITLE OF INVENTION: FOR THEIR USE
FILE REFERENCE: CLON-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT APPLICATION NUMBER: 00/211,607
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFFWARE: FREKSEQ for Windows Version 4.0
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                                                                                                                                                                                               Score 41.6; DB 16; Length
Pred. No. 0.003;
0; Mismatches 79; Indels
; OTHER INFORMATION: variant of sequence from Discosoma sp. US-10-315-920-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10315920 Publication No. US20030175809A1 GENERAL INFORMATION:
                                                                                                                                                                                                     Query Match 23.5%;
Best Local Similarity 53.0%;
Matches 89; Conservative
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Best Local Similarity 53.04
Matches 89; Conservative
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## APPLICANT: Labas, Yulii A.
## APPLICANT: Matt, Mikhail V.
## APPLICANT: Matt, Mikhail V.
## APPLICANT: Matt, Alexey
## TITLE OF INVENTION: No. US20/2019/6/6Alel Chromophores/Fluorophores and
## TITLE OF INVENTION: Methods for Using the Same
## TITLE OF INVENTION: Mother: US/10/006,922
## CURRENT APPLICATION NUMBER: US/12-0.
## PRIOR APPLICATION NUMBER: US/12-0.
## PRIOR APPLICATION NUMBER: US/45, 898
## PRIOR APPLICATION NUMBER: 09/459, 144
## PRIOR APPLICATION NUMBER: 09/459, 144
## PRIOR APPLICATION NUMBER: 09/459, 149
## PRIOR APPLICATION NUMBER: 09/459, 149
## PRIOR APPLICATION NUMBER: 09/459, 149
## PRIOR APPLICATION NUMBER: 09/449, 138
## PRIOR APPLICATION NUMBER: 09/450, 119
## NUMBER OF SEQ ID NOS: 46
## SEQ ID NOS: 46
## SEQ ID NOS: 46
## INCITED OF THE 
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TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and ittle OF INVENTION: Methods for Using the Same FILE REFERENCE: CLON-035CIP CURRENT APPLICATION NUMBER: US/10/006,922 CURRENT PILING DATE: 2001-12-04 PRIOR APPLICATION NUMBER: US/120,330 PRIOR FILING DATE: 1998-12-11 PRIOR APPLICATION NUMBER: 09/457,898 PRIOR FILING DATE: 1999-12-09 PRIOR PILING DATE: 1999-12-09 PRIOR PILING DATE: 1999-12-09 PRIOR FILING DATE: 1999-12-09 PRIOR FILING DATE: 1999-12-09 PRIOR FILING DATE: 1999-12-09 PRIOR PILING DATE: 1999-11-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 46
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lukyanov, Sergey A APPLICANT: Fradkov, Arcady F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Discosoma species
US-10-006-922-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-006-922-37
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                                                                                                                                                                                                                                                                                                                                                                                    Length 681;
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                                                                                                                                                                                                                                                                                                                                                        Query Match
23.5%; Score 41.6; DB 13;
Best Local Similarity 53.0%; Pred. No. 0.003;
Matches 89; Conservative 0; Mismatches 79;
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Job time : 405.323 secs
; TYPE: DNA
; ORGANISM: Discosoma species
US-10-006-922-37
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BF305332 CF1440841 AW500841 AW500841 CW278122 CW278118 CD611367 CM278116 CW278116 CG278116 CG278116 CG278116 AU132340 AU132340 AU1393108 BI333060 BM456185

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BP321118 BP266195

UI-HF-BPO UI-HF-BPO 328743034

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OM nucleic

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Run

Sequence:

Minimum DB Maximum DB

Database

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WOUND1 50 E10.g1 A002 Wounded leaves Sorghum bicolor cDNA clone WOUND1 50 E10 A002 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (Bases 1 to 786)

1 (Bases 1 to 786)

2 (Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Brady, J., Eastman, A., Miller, V., Gonzalez, M., Anfuso, C., Chhabras, D., Johnson, H., Kamran, D. and Pratt, L. H.

A Sorghum EST database: mechanically damaged and methyl jasmonate-treated leaves
Unpublished (2003)

Cother ESTS: WOUND1 50 E10.bl A002

Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mmprattedga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
Sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Far: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="WOUND1 50 E10 A002"
/lab host="DHIOB-T1 phage-resistant E. coli"
/clone_lib="Wounded leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: Sugs (CTTCTGCTTAAAAGCTGCG)
Location/Qualifiers
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AU139517
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BP266195
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2941
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RESULT 1
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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CF847742 psMA002xG
BG83616 2000 4011
BQ294408 1091028H0
BQ779473 946120G01
BI478941 949071B07
CA828471 111402B0
CA828471 111402B0
CB866436 3529 1_95
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CF635183 Zmrww00 0
CD446144 EL01T0208
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                                                                                                                                                                                                                                                                                            1 gccgacgtgccagggaacta.....acgagaacgtcaaggtgtga 177
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                              US-10-617-978-17_COPY_73_249
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                nucleic search, using sw model
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CB866436
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BU499682
CC635183
CC645144
CC371039
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psHB018xO20f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone sHB038020 5, mRNA sequence.
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                                                                                                                                                                                                                                                                                      CTGGGCGACAACCCGGACTGCATCAAGATCTGCCAGAAGCACGGCGTCGACTACGGCTAC
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/cell_line="P6497"
/dev_Eage="849 hr. post infection stage"
/lab_hoste="848 hr. post infection stage"
/lab_hoste="848 hr. post infection of Phycophthora sojae
                                                                                                                                                                                                                                      184 GGCGGTGGGGCTGAGCGCAAGAGCCCAACATGAACTACGACAAGCTGAGCCGCGCC
                                                                                                                                                                                      1 GCCGACGTGCCAGGGAACTACCCGCTGGACAGCTCGGACAACACCTGTGCGCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes during infection and propagation sHB"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xhol"
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Phytophthora.
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                                                                                          Length 632;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 304 CGCTTCGACTTCCAGGGCCTGGCGCAGTGCCTGCCAGCCG 343
                                                                                                                                                                                                                                                                                                                                                                                  121 TGCTACGCGTTCCAGTGTTGGTGCGAGTTCCTGAAGGACG 160
                    Note: this is a NIH_MGC Library."
                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1880 Pratt Dr., Blacksburg, VA 24061, USA Tel: 540-231-7318
                                                                                          DB 2;
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/organism="Phytophthora sojae"
/mol_type="mkn4"
/db xref="taxon:67593"
/clone="sHB038020"
                                                                                       Score 43.2; DB Pred. No. 0.19; 0; Mismatches
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CF846529.1 GI:38062183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bmtyler@vt.edu
                                                                                       ch
1 Similarity 54.4%;
87; Conservative
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Phytophthora sojae
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                                                                                                                Best Local Similarity
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CF846529
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Site_2: XhoI; The library was prepared from polyA+ RNA harvested from 8-day-old hydroponically grown, BTx623 sorghum seedlings. For some plants, one-half of the second leaf ws crushed without damaging the midvein. For others, methyl jasmonate was added to the growth medium to a final concentration of 100 uM. Leaves were harvested 3 and 27 hr after treatment and pooled. Double-stranded cDNA was cloned unidirectionally into different Draili sites of the PME18S-FL3 vector (5-prime Draili site is CACTGTGTG, insert."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE262829 632 bp mRNA linear EST 26-OCT-2000 601151586F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3507620 5',
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH10B (phage-resistant)"
/clone_lib="NH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
cloned into BoorsIX (site susing the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
california, Berkeley) using SAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCCAGAAGCACGGCGTCGACTACGGCTACTGCTACGCGTTCCAGTGTTGGTGCGAGTT 149
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 632)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCC
CONA Library Preparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I. M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                  30 CAGCTCGGACAACACCTACCTGTGCGCACCCCTGGGCGACAACCCGGACTGCATCAAGAT
                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                   Score 44, DB 7; Length 786;
Pred. No. 0.12;
0; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 27 High quality sequence stop: 616.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="mRNA"
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1 Similarity 57.1%;
80; Conservative
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Matches 80; Conserv
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446 bp mRNA linear EST 15-MAY-2002 Schmidt lab Zea mays CDNA, mRNA sequence.
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/tissue_type="Developing kernels (sibcrossed)"
/dev_stage="10-11 days post-silk emergence"
/clone_lib="Zm08_AAFC_ECORC_Fusarium_graminearum_inoculate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 TCATCCAGAACGTCCCCGACCGCAACGGCGACCGCTACGAGGCCATCTACAGCTTCTACT 247
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Beparatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d_corn_ear"

"f_notes_weetcr: Bluescript St+/XhoI-EcoRI; Site_1: EcoRI;
Site_2: XhoI: Field-grown maize ears were silk
channel-inoculated in the morning (-10 am) with 1 ml of s
Fusarium graminearum macroconidala suspension (500,000
spores/ml) and whole ears were collected and immediately
frozen in liquid nitrogen 6 days later."
    ZmOB_AAFC_ECORC_Fusarium_graminearum_inoculated_corn_ear Zea mays
cDNA_clone_ZmOB_04h11, mRNA sequence.
                                                                                                                                                                                                                                      Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A., Spott, D. and Tinker, N.A.
Expressed Sequence Tags from Developing Maize Kernels Six Days after Silk Channel Inoculation with Fusarium graminearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 ACAAGGTGTACAACGGCAGCCTGGACAAGCGGCTGGGCGTCACCGCGGGCATCTGCGTGC
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Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6
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                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.7%; Score 42; DB 4;
ilarity 55.5%; Pred. No. 0.41;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 TCCTGAAGGACGAGACGTCAAGGTG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/cultivar="CO430"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: (613) 759-1314
Pax: (613) 759-6566
Email: harrislj@agr.gc.ca.
Location/Qualiflers
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                                                 BG836816
BG836816.1 GI:14203139
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Matches 81; Conserv
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320 CCCAGCAGCTACGACGCCGGCTACGTGAGCCTGTCGGGGCTACGAGGGCTACGAAGAGGGGA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="mycelium"
/lab host="synthetic medium"
/clone lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation sMA"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xhol"
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hytophthora.
(bases 1 to 684)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1880 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyler@vt.edu
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|mol_type="mkNA"
|db_xref="taxon:67593"
|clone="sMA002G02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: BK reverse primer Plate: 002 row: G column: 02 Seq primer: BK reverse primer. High quality sequence stop: 684. Location/Qualifiers
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/cell_line="P6497"
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FORWARD: BK reverse primer
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Unpublished (2003)
Contact: Tyler B
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Phytophthora sojae
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/organism="Zea mays"
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                              location/Qualifiers
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946120501.y1 946 - tassel primordium prepared by Schmidt lab Zea
mays cDNA, mRNA sequence.
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ECORI; Site_2: XhoI; RNA from library 606 was filtered for
common ESTE_found in 606."
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/lab_host="Stratagene XLOLR"
/clone_lib="1091 - Immature ear with common ESTs screened
by Schmidt lab.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/tissue_type="Inflorescence meristem - floral organ
primordia"
                          1 (bases 1 to 446)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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Pred. No. 1.1;
0; Mismatches 66; Indels (
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Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                      Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="mRNA"
/cultivar="OH43"
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Fax: 650 725 8221
Email: walbot@stanford.edu
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BQ779473
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/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between Inm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a IKb average."
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949071B07.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose
Eam mays cDNA, mRNA sequence.
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/mol_type="mRNA"
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/db_xref="taxon:4577"
/db_vref="taxon:4577"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="946 - tassel primordium prepared by Schmidt
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/cultivar="W64A"
/db_xref="taxon:4577"
/tisbue_type="immature leaf primordium and vegetative
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/lab_host="E. coli XLOLR"
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Fax: 650 725 8221
Email: walbotogestanford.edu
Plate: 949071 row: B column: 07.
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Department of Biological Sciences
Stanford University
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/tissue_type="ear"
/tissue_type="ear"
/dev_atage="2 mm"
/lab host="E, coli XLOLR"
/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
                                                                                                                                                                                                                                                   29 ACAGCTCGGACAACACCTGTGCGCACCCCTGGGCGACAACCCGGACTGCATCAAGA
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Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
amplīfied. Ampicillin is the selection marker."
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                                                                                                   Score 40.4; DB 6; Length 617;
Pred. No. 1.1;
0; Mismatches 66; Indels
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Fax: 650 725 8221
Email: walbotgestanford.edu
Plate: 3529 1 95 1 row: F column: 01.
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/cultivar="B73"
                                                                                                       Query Match
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   selected."
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                                                           /note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site 1: ECORI; Site 2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
ECORI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing - includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."
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/note="This library represents the unique genes found in
the fourth round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 1091 and 3524. Contigs were assembled using
ZmDBAssembler and 2 representatives from each contig were
selected for the Unigene set. All singlets were also
/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve
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    (basee 1 to 617)

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Fax: 650 725 8221
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/db_xref="dbEST:1091028H08.y2"
/db_xref="taxon:4577"
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Plate: 1114028 row: F column: 02.
Location/Qualifiers
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Department of Biological Sciences
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/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between Imm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
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1 (bases 1 to 652)
Walbot, V.
                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
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/clone_lib="946 - tassel primordium prepared by Schmidt
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                                                                                                                                                                                                                                                                                                Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
815 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 227
Fax: 650 728 8221
Email: walbockestanford.edu
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/mol_type="mRNA"
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Contact: Walbot V
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946160D07.yl 946 - tassel primordium prepared by Schmidt lab Zea
BU098969
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1 (bases 1 to 624)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences Stanford University
Stanford University
B55 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227,
Fax: 650 725 8221
Email: walbordedstanford.edu
Plate: 946160 row: D column: 07.
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                    TCCTGAAGGACGAGAACGTCAAGGTG 174
                                                            424 rcccacacacacic 399
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/note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between Imm and 3mm. Sharon Stanfield prepared the CDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
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                                                                                                                                 /tissue_type="tassels"
/dev stage="just after the transition from vegetative to
inflorescence development"
/lab_hoste="XLOLR"
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/lab_host="B. coli XLOLR"
/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
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Fax: 650 725 8221
Email: walbot@stanford.edu
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/db_xref="taxon:4577"
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ilarity 54.8%;
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(bases 1 to 666)
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University
Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946134 row: C column: 03.
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Fax: 650 725 8221
Email: walbot@stanford.edu
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Stanford University
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/cultivar="0H43"
/db_xref="taxon:4577"
/tissue_type="tassels"
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                                       Query Match 22.8%; Score 40.4; DB 6; Length 668; Best Local Similarity 54.8%; Pred. No. 1.1; Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps
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Mesobuthus martensii
Bukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidae; Buthidae; Mesobuthus.

1 (bases 1 to 354)
Zeng, X.-C., Li, W.-X. and Zu, S.-Y.
A novel CDNA sequence encoding the precursor of a new type of insect beta-neurotoxin, BmKBT from Chinese scorpion Buthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-MX-1999) Department of Virology and Molecular Biology, Virology Institution of Wuhan University, Luojia Street, Winhan, Hubei 430072, P.R. China (15-MX-1999) Department of Wuhan University, Luojia Street, Winhan, Hubei 130072, P.R. China (15-MX-1999) Department of Virology and Molecular Biology, Virology Institution of Wuhan University, Luojia Street, Wuhan, Hubei 430072, P.R. China Sequence update by submitter Sequence update by submitter on Oct 6, 2004 this sequence version replaced gi:30844240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesobuthus martensii insect beta-neurotoxin (bt) mRNA, complete
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/db_xref="taxon:34649"
/tissue_type="venom gland"
/note="authority: Buthus martensii Karsch"
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/organism="Mesobuthus martensii"
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Li,W.-X., Zeng,X.-C. and Zu,S.-Y.
Direct Submission
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ARS66416 Sequence
AX061774 Sequence
AX061774 Sequence
AX061773 Sequence
ARS66413 Sequence
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Hottentotta judaica
Hottentotta judaica
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Hottentotta.
                                                                                                                                                                                                                                                                              PAT 08-OCT-2004
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      107 GACGATCCAGGAAATTATCCGACAAATGCTTACGGTAACAAATATTATTGTACGATTTG 166
                                                         66 GGAGATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGC 125
                                                                                              167 GGAGAAATGAATATTGTAGGAAAATATGTAAATTGCATGGAGTTACTTATGGTTATTGT 226
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/db_xref="taxon:6863"
                                                                                                                                                                                                                                                                              DNA
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Patent: US 6768002-A 34 27-JUL-2004;
Location/Qualifiers
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Sequence 34 from patent US 6768002.
AR566415.1 GI:53983405
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Sequence 34 from Patent WO0078957.
AX061772
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/mol_type="genomic DNA"
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Herrmann, R. and Wong, J.F.
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              /codon_start=1
/product."insect beta-neurotoxin"
/protein_id="AAPA1418.2"
/db_xref="G1:53828930"
/translation="MMKFLLFGMFVILFSLMGSIRGDDDFGNYPTNAYGNKYYCTILG
ENEYCRKICKLHGVTYGYCYNSRCWCEKLEDKDVTI"
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Mesobuthus martensii toxin KBT precursor, mRNA, complete cds.
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ENEYCRKICKLHGVTYGYCYNSRCWCEKLEDKDVTI"
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Mesobuthus martensii
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthioidae; Mesobuthus.
1 (bases 1 to 469)
Jiang, D., Cao, Z. and Li, W.
Cloning and characterizing of a new scorpion toxin from Buthus
                                                                                                                                                                                                                                                                                              81 GACGATCCAGGAAATTATCCGACAAATGCTTACGGTAACAAATATTATTGTACGATTTTG 140
                                                                                                                                                                                                                                                                                                                                     66 GGAGATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGTGTGGATTACGGGTATTGC 125
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Jiang,D., Cao,Z. and Li,W.
Direct Submission
Submitted (23-APR-2003) Biotechnology, College of Life Sciences, Luojia Mountain, Wuhan, Hubei 430072, China
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:34649"
/tisque_type="venom"
/country="China"
/note="authority: Mesobuthus martensii Karsch"
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                                                                                                                                                                           Length 354;
                                                                                                                                                                                                                  73; Indels
                                                                                                                                                                         Query Match 32.0%; Score 57.2; DB 3; Best Local Similarity 58.0%; Pred. No. 1.2e-07; Matches 101; Conservative 0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="toxin KBT precursor"
/protein_id="AAQ22733.1"
/db_xref="GI:33590393"
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/product="toxin KBT"
329. .334
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/note="BmKBT2"
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Best Local Similarity 58.0
Matches 101; Conservative
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mat_peptide
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Hottentotta judaica
Hottentotta judaica
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones;
Butkida, Buthoidea, Buthidae, Hottentotta.
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Hottentotta judaica
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Hottentotta.
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                                                                      PAT 24-JAN-2001
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                                                                      linear
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Herrmann, R., Lee, J.M. and Wong, J.F.
Scorpion toxing from buthotus judaicus
Patent: WO 0078957-A 32 28-DEC-2000;
E.I. DU PONT DE NEWOURS AND COMPANY (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hottentotta judaica"
/mol_type="unassigned DNA"
/db_xref="taxon:6863"
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Scorpton toxins from buthotus judaicus
Patent: WO 0078957-A 36 28-DEC-2000;
E.I. DU PONT DE NEWOURS AND COMPANY (US)
Location/Qualifiers
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Best Local Similarity 61.1%; Pred. No. 0.033;
Matches 66; Conservative 0; Mismatches 4
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/organism="Hottentotta jud
/mol_type="unassigned DNA"
/db_xref="taxon:6863"
                                                            270 bp
Sequence 32 from Patent WO0078957.
AX061770
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Sequence 36 from Patent WO0078957.
AX061774
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AX061774
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                131 ATCATGATTATTGTGCGGACATTTGTAAAGTACATGGAGTGAATTATGGGTATTGTTGGG 190
GAGATAATCCGGACTGCATTAAGATCTGTCAGAACACGGTGTGGATTACGGGTATTGCT
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                                                                    127 ACGCCTTCCAATGCTGGTGTAATTTCTGAAGGATGAGAACGTGAAGGTCT 177
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Pred. No. 0.033;
0; Mismatches 42; Indels
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Patent: US 6768002-A 32 27-JUL-2004;
Location/Qualifiers
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Herrmann, R. and Wong, J.F.
Scorpion toxins
Patent: US 6768002-A 36 27-JUL-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 bp
Sequence 36 from patent US 6768002.
AR566416
AR566416.1 GI:53983406
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Sequence 32 from patent US 6768002.
AR566414
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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Herrmann, R. and Wong, J.F.
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Best Local Similarity 61.17
Conservative 6; Conservative
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Matches 66; Conserv
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67
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AR566414
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AR566416
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316 bp mRNA linear INV 12-FEB-2004 Centruroides limpidus limpidus sodium-channel modifier toxin Cll7 AP491133
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/protein id="AAP49508.1"
/b_xref="G1:3137632"
/translation="WANSLANIACLVLFGTVWAKEGYLVNTYTGCKYICWKLGENKYCIDECKEIGAGYGYGYGGGYCEGFPENKPTWPLPNKTGGRK"
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Centruroides sculpturatus isolate CsEv1b beta-toxin gene, partial
                                                                                                                                                                                                                                        Centruroides limpidus limpidus
Centruroides limpidus limpidus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 TACCTGTGCGCCCCTTTGGGAGATAATCCGGACTGCATTAAGATCTGTCAGAAACACGGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 TACATTTGCTGGAAATTGGGAGAGAAAAATACTGCATTGATGAATAAGAGATAGGA 160
                                                                                                                                                                                                                                                                                                                1 (bases 1 to 316)
Corona, M. and Possani, L.D.
Genes and peptides from the scorpion Centruroides limpidus
limpidus, that recognize Na(+)-channels
Unpublished
2 (bases 1 to 316)
Corona, M. and Possani, L.D.
Direct Submission
Submitted (12-MAR-2002) Bioestructura y Reconocimiento Molecular,
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/note="encodes sodium-channel modifier toxin Cll7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="sodium-channel modifier toxin Cll7" 248. .250
/note="amidation site"
                     193 ACCTCGTGTTGGTGTGATATTTGAAAAAGAAGACATCGATATTT 238
132 TICCAATGCTGGTGTGAATTTCTGAAGGATGAGAACGTGAAGGTCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 3; Length 316;
Pred. No. 0.27;
0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Centruroides limpidus limpidus"
/mol_type="mRNA"
/mol_type="limpidus"
/dub_species="limpidus"
/db_xref="taxon:29941"
/mote="preproprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 GIGGATTACGGGTATTGCTACGCCTTCCAATGCTGGTGTAA 149
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Location/Qualifiers
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ilarity 60.8%;
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Best Local Similarity
Matches 62; Conserv
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AY351304.1
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misc_feature
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Buthida; Buthoidea; Buthidae; Hottentotta.
                                                      PAT 08-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGAAATTACCCGATATCTGTTTATGGTACTTTATGGATGCACGCTTTTAATCAT 135
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Pred. No. 0.28;
0; Mismatches 70; Indels
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                                                      linear
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Scorpton toxins from buthotus judaicus
Parent: WO 0078957-A 30 28-DEC-2000,
E.I. DU PONT DE NEMOURS AND COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                      DNA
                                                                                                                                                                                                   1 (bases 1 to 270)
Herrmann, R. and Wong, J.F.
Scorpion toxins
Patent: US 6768002-A 30 27-JUL-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                  AR566413 270 bp Sequence 30 from patent US 6768002.

    .270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX061768 270 bp
Sequence 30 from Patent WO0078957.
AX061768
                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
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ARS66413.1 GI:53983403
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21.2%;
Best Local Similarity 56.0%;
Matches 93; Conservative
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Hottentotta judaica
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                                                                                                                                                                  Unknown.
Unclassified.
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Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, B van
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
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Centruroides sculpturatus isolate CsEvle beta-toxin gene, partial
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Centruroides sculpturatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Centruroides.
1 (bases 1 to 192)
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    192
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                                                                                                                                                                      17;
                                                                                                                                        DB 3;
                                                                                                                                    Score 36.8; DB Pred. No. 0.69; 0; Mismatches
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Pred. No. 0.69;
0; Mismatches
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AY351306.1 GI:38017470
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20.6%;
Best Local Similarity 73.4%;
Matches 47; Conservative 0
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1 Similarity 73.4%;
47; Conservative
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Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
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Buthida; Buthoidea; Buthidae; Centruroides.

    (bases 1 to 192)

                          Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones, Buthida, Buthida, Buthidae, Centruroides.
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Centruroides sculpturatus isolate CsEvIc beta-toxin gene, partial
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Submitted (24-JUL-2003) Leuven University, Lab
Submitted, Leuven, Flanders 3000, Belgium
Evenstraat, Leuven, Planders
1. .192
/organism="Centruroides sculpturatus"

    192
/organism="Centruroides sculpturatus"

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2 (bases 1 to 192)
                                                                                                  Alignment of beta-toxin nucleotide sequences Unpublished 2 (bases 1 to 192)
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Centruroides sculpturatus
 Centruroides sculpturatus (bark scorpion)
Centruroides sculpturatus
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<1. .>192

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AY351305.1 GI:38017468
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Best Local Similarity '
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Zhu,S.
Direct Submission
Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
Evenstraat, Leuven, Flanders 3000, Belgium
Location/Qualifiers
1. 192
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                                                                                                     Centruroides sculpturatus (bark scorpion)
Centruroides sculpturatus
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthida, Buthoidea; Buthidae, Centruroides.
1 (bases 1 to 192)
2hu, S.
Alignment of beta-toxin nucleotide sequences
Unpublished
                AY351307 1902 bp DNA linear INV 31-DEC-2003
Centruroides sculpturatus isolate CsEv1d beta-toxin gene, partial
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